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# 202479 s at HG-U133A

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# 30 202863\_at HG-U133A

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#### 206461 x at HG-U133A

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#### 208646\_at HG-U133A

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#### 208651 x at HG-U133A

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#### 209061\_at HG-U133A

#### 209062\_x\_at HG-U133A

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#### 209085 x at HG-U133A

#### 209101\_at HG-U133A

### 20 209135\_at HG-U133A

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### 209160\_at HG-U133A

#### 209167\_at HG-U133A

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#### 209168\_at HG-U133A

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## 212236\_x\_at HG-U133A

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### 213772\_s\_at HG-U133A

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#### 213891 s at HG-U133A

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## 20 214315\_x\_at HG-U133A

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## 214321\_at HG-U133A

## 214394\_x\_at HG-U133A

214395\_x\_at HG-U133A

## 214430\_at HG-U133A

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#### 214439 x at HG-U133A

#### 214450 at HG-U133A

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# 214693\_x\_at HG-U133A

# 15 214700\_x\_at HG-U133A

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#### 35 215215 s at HG-U133A

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#### 215622\_x\_at HG-U133A

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#### 216449 x at HG-U133A

216450\_x\_at HG-U133A

## 216609\_at HG-U133A

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## 216640\_s\_at HG-U133A

#### 216652 s at HG-U133A

## 216680\_s\_at HG-U133A

### 216698\_x\_at HG-U133A

## 216833\_x\_at HG-U133A

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# 40 217225\_x\_at HG-U133A

#### 217375 at HG-U133A

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217504\_at HG-U133A

#### 217520 x at HG-U133A

# 217521\_at HG-U133A

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# 231873\_at HG-U133B

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# 235061\_at HG-U133B

### 235101\_at HG-U133B

## 235124 at HG-U133B

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#### 235259\_at HG-U133B

#### 235263 at HG-U133B

#### 235278\_at HG-U133B

### 235287\_at HG-U133B

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### 235719\_at HG-U133B

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#### 235749\_at HG-U133B

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# 235823\_at HG-U133B

20 actga

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### 236190\_at HG-U133B

# 40 236226\_at HG-U133B

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# 236280\_at HG-U133B

### 236293\_at HG-U133B

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# 236301\_at HG-U133B

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PCT/EP02/12303 WO 03/039443

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V	VO 03/039443		PCT/EP02/12303
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<b>#</b>	<u>의</u>	at	
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WO 03/039443		· PCT/EP02/12303
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WO 03/039443	PC I/EP0	2/12303
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WO 03/03944.		PC1/EP02/12303
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21344/ at		213370_s_at		
gp/Aio/2341	2000	gb BF057298		
COOR COMPANY OF THE PROPERTY O	Consensus includes gb.Aio / 234 i / F.Co. P.Co. Aid / F.Co. Aid / F.Co. P.Co. P.Co. P.Co. Aid / F.Co. P.Co.	ggaggaaggccattagcatctaaaaattgaagttgaagctgagttgaaactaggaagga	Consensus includes gb:BF05/298/FCA=E31/DB_ARCE 191.1001.1001.1001.1001.1001.1001.1001.	atatagagatttgaggaaagttatatccactaggtggcagtcattgatcataataagtgaaattgagcccttgttctngtacatgantttaggcttaggtaattaggtatgtgaaattacattcatt

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gb BF439472	gb Al554300	gb NM_000732.	
Consensus includes gp:BF439472/FEN-LOT IND-XNET grade (CLONE=IMAGE:3272361 /UG=Hs.29189 ATPase, Class VI, type //CLONE=IMAGE:3272361 /UG=Hs.29189 ATPase, Class VI, type //CLONE=IMAGE:756744 //UG=Hs.129943 KIAA0545 //CLONE=IMAGE:756744 //UG=Hs.129943 KIAA0545	Consensus includes gb:Al554300 /FEA=EST /DB_ARET-9:.***PRODUCTORS** /UG=Hs.183583 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member /UG=Hs.183583 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member /UG=Hs.183583 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member /UG=Hs.183583 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member /UG=Hs.183583 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member /UG=Hs.183583 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member /UG=Hs.183583 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member /UG=Hs.183583 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member /UG=Hs.183583 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member /UG=Hs.183583 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member /UG=Hs.183583 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member /UG=Hs.183583 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member /UG=Hs.183583 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member /UG=Hs.183583 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member /UG=Hs.183583 serine /UG=Hs.183583 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member /UG=Hs.183583 serine /UG=Hs.183	Consensus includes gp.Nw_ooc/32. (CD3D antigen, delta polypeptide (TiT3 complex) /DB_XREF=gi:4502668 /UG=Hs.95327 /FEA=CDS /GEN=CD3D /PROD=CD3D antigen, delta polypeptide (TiT3 complex) /CD3D antigen, delta polypeptide (Ti	ggacattctggggaactgggcaccaggagtgccttcatacactgtaccccagctcttaaaagagaaagaa

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213725 x at	213716 s at	213689_x_at	
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213922 at gb AW294686	·
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chi	gb A1744627	gb AA053830	ablAW589975	gb BG236220
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214109 at	214051_at	214030_at
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Consensus includes gb:NM_001335.1 //DEF=Homo sapiens cathepsin W (lymphopain) (C I SW), mkn/k. / FEA=C/D3 //GEN=CTSW //PROD=cathepsin W (lymphopain) //DB_XREF=gi:4503156 //JG=Hs.87450 cathepsin W (lymphopain) //FL=gb:AF013611.1 gb:NM_001335.1 agactigacacggcatigacctgactgacctgactgacctgac	gannnnanligtggagtctgcngganggagtgcaaacgtaccctgntnngnaticaggcn gnggnaggnnnctnctcaaagcccnnnnnnnnnnnqngtigaatgtccagag grapgagtctgcggtctggaacagccconnnnnnnnnnnnnqngtigaatgtccagag atroggggcctgggactagaacattccacaaggagatgagcacacatcaagtcaaccagaacctcaaat gattgtcggcctggagaacatcaacacgggagtcaacacttcacgtccaagtccaaccagaacctcaat gatgtgtggtggtcggctcggaacaagggaacaaggaccttcagtccaagtgatgatgagtcaacaggccagggccagggccagggccagggccagggccaggagcacacttcaggccaggagccaggagccagggcgcacacacagaagggccagggcgggggg

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217419 × at	217418_x_at	
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Consensus includes gb. AK02/1586. 1/IDEF=Homo sapiens cDIVA FL. I 1524 its, croite network in light sepiens agrin precursor mRNA. FEA=mRNA /IDE XREF=gj:10432794 /IDG=Hs.27330 Homo sapiens, clone IIMAGE:3506210, mRNA, partial cds atcoccagcagcaccagggccogtigtaccaggcccagtigtaccaggcccaggcaggidgcaggaaltiqueltiguaggaacagggcaggcaggcaggcaggcaggcaggcagg	Consensus includes gb:X12530.1 /DEF=Human mRNA for B lymphocyte antigen CD20 (p1, pp3). If EX-III (NA) /DB_XREF=gi:29773 /UG=Hs.89751 membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for	ctggcgtcttcaccaccatggagaaggctggggctcatttgcagggggggg

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Contains a pseudogene similar to ribosomal protein L26, STSs and GSSs /FEA=CDS /DB_XREF=gi:6855342 /UG=Hs.272344 Contains a pseudogene similar to ribosomal protein L26, STSs and GSSs /FEA=CDS /DB_XREF=gi:6855342 /UG=Hs.272344 Contains a pseudogene similar to ribosomal Human DNA sequence from clone RP13-258015 on chromosome Xq21.2-Xq21.33 Contains a pseudogene similar to ribosomal protein L26, STSs and protein L26, STSs and GSSsatgaagtttaatccttttgtgacttccaactgaaggaagaggtgaaaaggctgaaaaggctgaaaaggctgaaaaggctgaaaggctgaaaaggctgaaaaggctgaaaaggctgaaaaggctgaaaaggctgaaaaggctgaaaaggctgaaaaggctgaaaggctgaaaggctgaaaggctgaaaggctgaaaggctaaaggctaatggcacaaattgaacgggtgatcaactggcaaaaggctgaaaaggctgaaaggccgcaaaggcacaaaggctgaaaaggctgaaaaggccgcaaaggcaaaaggctgaaaaggccgcaaaggcaaaaggcgcaaaaggcgcaaaaggccgcaaaaggcgcaaaaggccgcaaaaggcgcaaaaggccgcaaaaggccgcaaaaggccgcaaaaggcggaaaaaggccgcaaaaggccgcaaaaggccgcaaaaggcgggggg	Consensus includes gb:AK02362b.1 / Int==Homo sapieris curva Ft1 3000 insperies ft. 28880 PAN2  PROBABLE OXIDOREDUCTASE (EC 1) / FEA=mRNA / IDB_XREEF=gi:10435607 / IUG=Hs.28880 PAN2  proteiniteateiticagateitgateitattitititititititititititititititit	Ignatgactgagtgagtgaatgaatgaagcctctgactttccagcctctccgccattgctccactaacta

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Consensus includes gic.Nov.249 13.17.021 Homo sepiens cDNA; FLI21260 fts, clone  COL0144 1gngnnnaanngtgntgactagognnttaagaacttgagagtanaagcaacataagatttttacctctctcgttccaccccaaactgaggacttaagttttgtttg	Consensus includes gb:BF343862 /FEA=ES1 /DB_XREF=gi:11291001 /DB_XREF=gi:01291001 /DB_XREF=gi	atagcagagggggttttatgcaaacgcactcacctocgccttggggaatgaaagggtcacttctgcatcactagctag

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CONSENSUS Includes go. br 360.7 / JUG=HS, 18585 ESTs, Moderately similar to ALU4_HUMAN ALU SUBFAMILY SB2 SEQUENCE (CONTAMINATION WARNING ENTRY  CONTAMINATION WARNING ENTRY  H. sapiensgatcagacctgtaataggatgaatttccatgcacttaacatgaagagatacaaaaagaatctaggacgagatatatat	Consensus includes gb:AW170571 /FEA=ES1 //DB_XREF=gi:D4U2096 //DB_AREF=est:Mibol 1 i.X 1 /CLONE=minosition (UG=Hs, 96144 copine)  (Ug-Hs, 96144 copine)  (Ug-Hs, 9614 copine)  (Ug-Hs, 961 copine)  (Ug-Hs, 961 copine)  (Ug-Hs,	taagctgttctgtttctgtggctttaactgacatatttctgtagcatctgccttcatctcatctcagcgtaatgaaatattaatgaaatcgctgaaaaagctttgccttcgagagggccagaagcct cgcggaatgtctgcaagtccaaagacgcgtgtgggttgtgccctgaagtgccgtccagcaggcggtgtgggccggacggccggc

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Consensus includes gb:BE85/99/FEA=ESI/DB_XKEF=gi:1038049/DB_XKEF=est./gu/av/.xi/CEONE=IMAGE.330746/UG=Hs.205293 KIAA1211  proteinggaggctgagggatgggaagaggctggaacagcaggaggcggaggtgcagggggcccccgagggcgtggaggagacctgggggaggccgcgggggggaaaagaggggcgccggggggg	Consensus includes gb:AW003297 /FEA=EST /DB_XREF=gi:5850213 /DB_XREF=est:wq65b01.x1 /CLONE=IMAGE:2476105 /UG=Hs.174104  ESTstgaaatgtgttggttacccatatctgatggaaatatgcagttggaagtcagatgcagtcgaagtcaacataagttgccaaagggagagatgtttttaacattcaggagaaattattcatctgatggaaatatgcagttggaagtcagttggaagtcagaagtcggttaatagttttcatcaaaattattcattc	4837 /FEA=EST /DB_XREF=gi:977 3=Hs. 119960 DKFZP727G051 ccccacgggcggacactcggccgggcagccccgtgtcanggggaagctgatggagaatcgagccaaagacttgatgtccaaactgacggaggtccgtgactttcgaagataattccaaatactgggtccttgaatgagatcctcatctgcggtgaggtgagcttccatcatcagggtgagcattagcgcggctttggaggctttggagagctttcatcaaacgggaccaataaatgagctttactattaaaaacggggaccaataaaatgatgtgtgctttactattaaa	tgttttnaatganaanaaaaaaaaaa

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Consensus includes gir.Ac.204901/DEF—nullian IDMA sequence in the control of in clinic insuling bir.Ac.20401/DEF—nullian in signer for two isoforms of a novel transcription factor similar to early B-cell factor (EBF) /FEA-mRNA_2 /DB_XREF—gi:990894 /UG=Hs.240559 Human DNA sequence from clone RP11-234G16 on clinic some 10. Contains ESTs, STSs, GSSs and CpG islands. Contains a gene for two isoforms of a novel transcription factor similar to early B-cell factor. Contains ESTs, STSs, GSSs and CpG islands. Contains a gene for two isoforms of a novel transcription factor similar to early B-cell factor. Contains ESTs, STSs, GSSs and CpG islands. Contains a gene for two isoforms of a novel transcription factor similar to early B-cell factor. Contains ESTs, STSs, GSSs and CpG islands. Contains a gene for two isoforms of a novel transcription factor similar to early B-cell factor. Contains ESTs, STSs, GSSs and CpG islands. Contains a gene for two isoforms of a novel transcription factor similar to early B-cell factor. Contains a gene for two isoforms of a novel transcription factor similar to early B-cell factor. Contains a gene for two isoforms of a novel transcription factor similar to early B-cell factor. Contains a gene for two isoforms of a novel transcription factor similar to early B-cell factor. Contains a gene for two isoforms of a novel transcription factor similar to early B-cell factor. Contains a gene for two isoforms of a novel transcription factor similar to early B-cell factor. Contains a gene for two isoforms of a novel transcription factor similar to early B-cell factor. Contains a gene for two isoforms of a novel transcription factor similar to early B-cell factor. Contains a gene for two isoforms of a novel transcription factor similar to early B-cell factor. Contains a gene for two isoforms of a novel transcription factor similar to early B-cell general general general general ge	gaggcctaaagtttaaaattaaaatttacnttcntgatgttttaattaaaatgtttgccacattaactttctgatgccttaaaagtgaaccttctttaaagaacctttgtgctatttatcacaggctt acactacaattgttaaaataaaa

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WO 03/039443				PCT/EP02/12303
228827_at		228766_at	228737_at	
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WO 03/039443			PCT/EP02/12303
228984_at	228916_at	228904_at	228834_at
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Consensus includes gb:AB037815.17DEF=Homo sapielis IIIRNA for NAA 1394 protein, particle Cos. 77 CATILLA (GEN=KIAA1394 /PROD=KIAA1394 protein /DB_XREF=gi:7243168 /UG=Hs.32156 KIAA1394 /PROD=KIAA1394 /PROD=KIAA1394 protein /DB_XREF=gi:7243168 /UG=Hs.32156 KIAA1394 /PROD=KIAA1394 /PROD=KIAA1394 /PROD=KIAA1394 protein /DB_XREF=gi:7243168 /UG=Hs.32156 KIAA1394 /PROD=KIAA1394 /PROD=KIAA13	Consensus includes gb:BE857467 /FEA=EST /DB_XREF=gi:103/1522/DB_XREF=est:779/011.X1/CLONE=IMAGE.304903/UG=Hs.24380  /UG=Hs.24380  EST scaggtcacaggcagaagagtcacagcagcagcagcatgctctggtcagtgacaactgtacatcaggagattgtgttgttttcttcttcacctgctcctatctat	Consensus includes gb:AW510657 /FEA=EST /DB_XREF=gi:7148735 /DB_XREF=est:hc89b09:X1 /CLONE=IWAGE:2907 for /UG=Hs.156044  ESTscaggatggtgagagatcctgaaagagctgcctatattataaattatatacatttttttaaggaaaagtgtgggggggg	Consensus includes gb:BF240286 /FEA=EST /DB_XREF=gi:11154209 /DB_XREF=est:601905816F1 /CLONE=IMAGE:4133978 /UG=Hs.178137 transducer of ERBB2, 1cgtggtngcggtggctgggctggctgctgctgttgctgtggctgctg

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228988_at gb AU157017		
Consensus includes gb:AUT570177EA=EST70B_XREF-9FF070B27REF - Consensus includes gb:AUT570177EA=EST70B_XREF-9FF070B27REF - Consensus includes gb:AUT570177EA=EST70B_XREF-9FF070B27REF - Consensus includes gb:AUT570177EA=EST70B2XREF-9FF070B27REF - Consensus includes gb:AUT570177EA=EST70B2XREF-9FF070B27REF - Consensus includes gb:AUT570177EA=EST70B27REF-9FF070B27REF - Consensus includes gb:AUT570TF070B27REF -	glyantagyccachighagagydrightiquegocagorigocagrighteaglyagyccochiaagycacaachtcocycocagagyaagyccighagagygycgagycagycgightiquegocagagyagycgcaaaachtcocycocagagyaagycdigyacagycagycagycgightiquegocagycgightiquegocagagycgightiquegocagagycgightiquegocagagycgightiquegocaga	accettgggtgacttaatgtgcccactggcccaagacctaccaagacctaccacttctgccctctcaggctctccagggtccaggtgggattgcccagggttggcccagggtgggattgcccaagggctctaggcctgccaagacctaccacttctgccctctaggctgctcctggattgcccagggtgccctggattgcccaggggtgccctggattgcccagggtgccctggattcccagggctgcttccaggattgccctggattgcccagggtgccctggattgcccagggttgcccaggattcccagggtgcccagggtgcccagggttgcccaggattcccagggttgcccaggattgccctggattgccctggattgccctggattgccctggattgccctggattgccctggattgccctgtctgcagattgcctttctgcctgtgctgtgattgccaggattgccctggattgccctggattgccctggattgccaggattgccctggattgccaggattgccctggattgccaggattgccctggattgccaggattgccctggattgccaggattgccaggattgccaggattgccaggattgccaggattgccaggattgccaggattgccaggattgccaggattgccaggattgccaggattgccaggattgccaggattgccaggattgccaggattgccaggattgccaggattgccaggattgcagcaggattgcaggattgcaggattagatt

WO 03/0394	43		PCT/EP	202/12303
229070_at	229061 s_at	229003_x_at	229001_at	
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	<b>WO</b> 03/0394	43					PCT/EP02/1230	)3
229253_at	229232_at		229194_at	229168_at	229138 at		229072_at	
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WO 03/039443		PCT/EP02/12303
229302 at	229280 s at	
gb AA058832	gb AK026189.1	
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WU (13/(139443			FC 1/EF02/12303
229368 s at	229362 at	229344 x at	229310_at
gb Al658995	gb AA878516	gb AW135012	gb BE465475
tgtacaga tcctagga cactaagt agccggg	Consensus includes gb:AA878516 /FEA=ES1 /DB_AREF-9i.2907401 /UG=Hs.112830 ESTs, Moderately similar to R3HU12 ribosomal protein S12, cytosolic /UG=Hs.112830 ESTs, Moderately similar to R3HU12 ribosomal protein S12, cytosolic /UG=Hs.112830 ESTs, Moderately similar to R3HU12 ribosomal protein S12, cytosolic /UG=Hs.112830 ESTs, Moderately similar to R3HU12 ribosomal protein S12, cytosolic /UG=Hs.112830 ESTs, Moderately similar to R3HU12 ribosomal protein S12, cytosolic /UG=Hs.112830 ESTs, Moderately similar to R3HU12 ribosomal protein S12, cytosolic /UG=Hs.112830 ESTs, Moderately similar to R3HU12 ribosomal protein S12, cytosolic /UG=Hs.112830 ESTs, Moderately similar to R3HU12 ribosomal protein S12, cytosolic /UG=Hs.112830 ESTs, Moderately similar to R3HU12 ribosomal protein S12, cytosolic /UG=Hs.112830 ESTs, Moderately similar to R3HU12 ribosomal protein S12, cytosolic /UG=Hs.112830 ESTs, Moderately similar to R3HU12 ribosomal protein S12, cytosolic /UG=Hs.112830 ESTs, Moderately similar to R3HU12 ribosomal protein S12, cytosolic /UG=Hs.112830 ESTs, Moderately similar to R3HU12 ribosomal protein S12, cytosolic /UG=Hs.112830 ESTs, Moderately similar to R3HU12 ribosomal protein S12, cytosolic /UG=Hs.112830 ESTs, Moderately similar to R3HU12 ribosomal protein S12, cytosolic /UG=Hs.112830 ESTs, Moderately similar to R3HU12 ribosomal protein S12, cytosolic /UG=Hs.112830 ESTs, Moderately similar to R3HU12 ribosomal protein S12, cytosolic /UG=Hs.112830 ESTs, Moderately similar to R3HU12 ribosomal protein S12, cytosolic /UG=Hs.112830 ESTs, Moderately similar to R3HU12 ribosomal protein S12, cytosolic /UG=IMAGE:2251894	Consensus includes gb:AVV13012 / FEA=E31 / DB_ANET - yi. O 1000 / DB	Consensus includes gb:BE465475 /FEA=EST /DB_XREF=gi:9511250 /DB_XREF=est:hw20g02.x1 /CLONE=IMAGE:3183506 //UG=Hs.272572 hemoglobin, alpha //UG=Hs.272572 hemoglobin, alpha //Ccattccagggcaggacatgctgccactgngctgttgagttga

WO 03/039443			PCT/EP02/12303
229513_at	229487 at	229420_at	229383_at
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Consensus includes gb:AK025613.1 / DEF=Homo sapiens CDNA: FLJ21960 fis, clone //DB_XREF=gi:10438184 / UG=Hs.287687 Homo sapiens cDNA: FLJ21960 fis, clone //DB_XREF=gi:10438184 / UG=Hs.287687 Homo sapiens cDNA: FLJ21960 fis, clone HEP05517tttgctgggattcattgaagggtcccttccttccattcatt	Consensus includes gb:W73890 /FEA=ESI /DB_XREF=gi:1382285 /DB_XREF=est.2005/02-SI /CEORE-invitorio-consensus includes gb:W73890 /FEA=ESI /DECA=ESI /DECAESI /DECA=ESI /DECAESI /DECA	aagcatco stigitiggol sigcicitico stitaaago	cgtcgagcgtggccgggacacgccggagctcgggaagtgggaggagggag

WO 03/039443			PCT/EP02/12303
229637_at	229621 x at	229575_at	·
gb AA166891	gb N93227	gb]AW271460	
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<b>WO</b> 03/0394			•	CT/EP02/12303
229745 × at	229722_at	229711_s_at	229681_at	229659_s_at
nhi Al 1468629	gb BF115733	gb AA902480	gb AW449289	gb BE501712
Consensus includes gb:Al468629 /FEA=EST /DB_XREF=g::4330 / 19 /DB_XREF=est:tn83g03.X1 /CLONE=iw/AGE.2123000 //UG=Hs.134185 ESTs, Weakly similar to 5E5 RAT 5E5 ANTIGEN //UG=Hs.134185 ESTs, Weakly similar to 5E5 RAT 5E5 ANTIGEN R.norvegicustcgctggcgctcgattcgctctcnccgnaacccccgccgacgcctcccgcaggcccccaggcgtcccaggggcccaggggcccaggggcccaggggcccaggggcccaggggcccaggggcccaggggcccaggggcccaggggccgacgcggggcccatcggcgccatcggcccatcggcccatcggcgccatcggggcccatcggggcccatcggggcccatcggggcccatcgcccatcgccatcgcccatcgcccatcgcccatcgccatcgcccatcgcccatcgccatcgcccatcgcccatcgcatcgccatcgccatcgccatcgccatcgcatcatcgccatcatcgccatcatcgccatcgccatcgcatcatcgccatcgcatcgcatcatcgccatcgcatcgcatcgcatcatcgcatcatcgca	Consensus includes gb:BF115733 /FEA=EST /DB_XREF=gi:10985209 /DB_XREF=est:/nb4a10.X1 /CLONE=IWAGE-3509202 /UG=Hs.87329 HSPC072 /UG=Hs.87329 /UG=Hs.	Consensus includes gb:AA902480 /FEA=EST /DB_XREF=gi:3037603 /DB_XREF=est:0K/0n12.51 /CLONE=IWAGE: 19 1930 / /UG=Hs.332938 carboxypeptidase //UG=Hs.332938 carboxypeptidase Maaattattgacttatttttatataaggtcactccgatgaaaggtgattacaaaatcatcacattgctnnnnnnnnnn	Consensus includes gb:AW449289 /FEA=EST /DB_XREF=gi:6990065 /DB_XREF=est:UI-H-Bi3-akn-r-U9-U-U-ST //CLONE=IMAGE:2734241 /UG=Hs.17551  //CLONE=IMAGE:2734241 /UG=Hs.17551  ESTsaggagaatcgcttgaacccgggaggggggttgcggttgcggttgagatcacgccactgcactccagcctgggcgacagannnnnctnngtcncaaaaacaaaaacaacaacaacaacaacaacaaccagggagga	/UG=Hs.205126 Homo sapiens cDNA: FLJ22667 fis, clone HSI08385tttttttggtggcaatcacagtctttaatcattnaattgtcatatttctgatttgttagcaagtgccagcttgtaggctggttgaagtacagaactcagaggaaaaaaaa

WO 03/039443		PCT/EP02/12303
229790 at	229779_at	229750 at
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WO 03/039443		PCT/EP02/12303	
229844_at	229833 at	229817_at	
gb Al699465	gb BF507533	gb Al452715	
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WO 03/039443		,	PCT/EP02/12303
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/UG=Hs.171395 Homo sapiens cDNA FLJ12049 fis, clone /UG=Hs.171395 Homo sapiens colored col	Rabb.interacting proteincaaggaccocacgoctgtgtctctgtgacaggaccaagggccagggncttcocacaaccaaaccaagcactcagcattcaaggaggttcaaaattcaaggagn proteincaaggaccocacgoctgtgtctctgtgaagagtcaaaagggccaaaggccaaaggccaaaggactaccaaaggaattcaaaaccaaaaacctaagcattcaagaagtactcaaaggagttcaaaattcaaaggagn innnatttccctagatgatgtgttctattgaggactactaaggaccaaggccaaaggccaaaggccaaaggccaaaggcaattcaaggaattcaaaaagaattcaaaaggaattcaaaaagaattcaaaggaattcaaaaggaattcaaaaagaattcaaggaattcaaaaaaaa	Consensus includes gb:AL353944.1 /DEF=Homo sapiens mRNA

V	VO (13/(139443		FC 1/E1 02/125	
232641_at	232636 at			
gb AC004908	gb AL080239			
/UG=Hs.249181 Homo sapiens PAC clone RP5-	XQ26.3-28 Contains part of a gene similar to IGFALS (insulin-like growth factor binding protein, acid labile subunit), an EST, SCSSs and a CpG Islandattititictituaticagaagcatacagtitytitytigattycaatgagaagtitictigagitytititytyattycagtycaatacagtitytytytictigattycaatacagtitytytytictigagitytaatacattitaatacattitaaacattyaagaatacattityaagtiticaagagagitytictigagityaagaacaaataattiticagacaataataattiticagatytyaacaaaataattiticaaataataattittaaaataaata	Consensus includes gb:AL080239 /DEF=Human DNA sequence from clotte Go 1-250022 on chromosome part of a gene similar to IGFALS (insulin-like growth factor binding protein, acid labile subunit), an EST, STSs, GSSs and a CpG part of a gene similar to IGFALS (insulin-like growth factor binding protein, acid labile subunit), an EST, STSs, GSSs and a CpG part of a gene similar to IGFALS (insulin-like growth factor binding protein, acid labile subunit), an EST, STSs, GSSs and a CpG part of a gene similar to IGFALS (insulin-like growth factor binding protein, acid labile subunit), an EST, STSs, GSSs and a CpG part of a gene similar to IGFALS (insulin-like growth factor binding protein, acid labile subunit), an EST, STSs, GSSs and a CpG part of a gene similar to IGFALS (insulin-like growth factor binding protein, acid labile subunit), an EST, STSs, GSSs and a CpG part of a gene similar to IGFALS (insulin-like growth factor binding protein, acid labile subunit), an EST, STSs, GSSs and a CpG part of a gene similar to IGFALS (insulin-like growth factor binding protein, acid labile subunit), an EST, STSs, GSSs and a CpG part of a gene similar to IGFALS (insulin-like growth factor binding protein, acid labile subunit), an EST, STSs, GSSs and a CpG part of a gene similar to IGFALS (insulin-like growth factor binding protein, acid labile subunit), and IGFALS (insulin-like growth factor binding protein, acid labile subunit).	gtagaatatgaccttcacctcatttctttcctcaagtgtatctggacgtatttggcttttgggcagtgncntgatgaaaagcaaaaatgaagaaaagaa	tagaccaactcaacagaattcttgctgaaggcaggccagggtgataagatatcaagagttaggggtgaggacagataccaagggtggagaaattttcactaaaactagtaggattttg gcttaaactggattctataagacagaaaaaggaagcccaaggtcaggtctagtggaagagaggctccggggagcccgacctgagtttgatctaggagagtctttgtcaatatcct

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/DB_XREF=gi:10439673 /UG=Hs.152432 Homo sapiens cDNA: FLJ23097 fis, clone	I/DB_XREF=gi:10437927_I/UG=Hs, 318722 Homo sapiens cDNA: FLJ21766 fis, clone I/DB_XREF=gi:10437927_I/UG=Hs, 318722 Homo sapiens cDNA: FLJ21766 fis, clone I/DEF7179atatictiggicaticaticatic gagaciticatic gagacitic ga	855D21gattccatgaccttcgaggatatccattgtagacttcactcaagaaggtgggccctgctgggacacatccagagaaagttgutucadgatygatyagaagattccatcaagaagattgactcaagaagattgatt

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232950 s at	
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Consensus includes gb:ABU40890.1 I/I/EF=PoiII/O septents in INVA POR POPENT AND A 1457 /PROD=KIAA1457 protein /DB_XREF=gi:7959174 /UG=Hs.272759 kiAA1457 yilloge-gas-gas-gitytic-gas-gas-gitytic-gas-gas-gitytic-gas-gas-gitytic-gas-gas-gitytic-gas-gas-gitytic-gas-gas-gitytic-gas-gas-gitytic-gas-gas-gitytic-gas-gas-gitytic-gas-gas-gitytic-gas-gas-gas-gitytic-gas-gas-gas-gas-gas-gas-gas-gas-gas-gas	LNG07418tatccccatgttacaaatgaagaaactgaggctcagagggagaaaaggggtccaaggtcatagagtgagt

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233072_at		
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233177 s at	233138_at
gb AB033010.1	gb[AU155968
Consensus includes gb:AB033010, 1/DEF=Homo salpietis linkiva for NAC 104 protein. Part of Nacion 194 (PROD=KIAA1184 protein / De_XREF=gi:6330254 /UG=Hs, 100747 KIAA1184 protein/De_KIAA1184 protein/De_KIAA1184 protein/De_KIAA1184 protein/De_KIAA1184 protein/De_KIAEF=gi:6330254 /UG=Hs, 100747 KIAA1184 protein/De_KIAA1184 protein/De_KIAEF=gi:6330254 /UG=Hs, 100747 KIAA1184 protein/De_KIAEF=gi:6330254 /UG=Hs, 100747 KIAA1184 protein/De_KIAA1184 protein/De_KIAEF=gi:6330254 /UG=Hs, 100747 KIAA1184 protein/De_KIAEF=gi:6330254 /UG=Hs, 100747 KIAA1184 protein/De_KIAEF=gi:6330254 /UG=Hs, 100747 KIAA1184 protein/De_KIAEF=gi:6330254 /UG=Hs, 100747 KIAEF=gi:6330254 /UG=Hs, 1	Consensus includes gb:AU155968 /FEA=EST /DB_XREF=gi:11017489 /DB_XREF=est:AU155968 /CLONE=PLACE1001745 //UG=Hs.178533 Homo sapiens cDNA FLJ13412 fis, clone  PLACE1001745gatgccactccangcigacqggctcgigaqqtctgcattcgagggattccatccactcacagatcatcacggctcqcctccangcigacqggctcqigaqqtctgcattcacqggattccactcacqtcacqtcactcacqgatcactcacqgatcactcacqgatcactcacqgatcactcacqgatcactcacqgatcactcacqgatcactcacqcactcacttattattgtcattgaaaaacttacactgcactcacqtcacq

WO 03/039443		PCT/EP02/12303
233328 x at	( <del></del>	233195 at
gb AL121673	gb AU145682	gb)AL117535.1
Consensus includes gb:AL 12 to 7 / DET - Filling DVA Sequence of the control of t	Consensus includes gb:AU145682 /FEA=EST /DB_XREF=gi:1100/203/DB_XREF=est:AU145682 /FEA=EST /DB_XREF=gi:1100/203/DB_XREF=gi:1100	tctgccctgggccaaaagggcccttcttgccaggggagagacagccacggtctctttggccgatgctgtattctcattttggcccttgttcttaggcccgtctgcccgccc

W U U3/U39443	FC1/EF02/12303
233483 at	
gb AK024458.1	
titicititititititititititititititititit	Consensus includes gb:AK024458.1 /DEF=Homo sapiens mRNA for FLJ00050 protein, partial cds. /FEA=mRNA /GEN=FLJ00050 /PROD=FLJ00050 protein /DB_XREF=gi: 10440429 /UG=Hs. 193857 Homo sapiens mRNA for FLJ00050 protein, partial cds. /FEA=mRNA for FLJ0

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233555_s_at	233520 s at	233500 x at
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Consensus includes gb.AL0344 to /DET - Itulian DIVA sequence from Script in 1975 to 19	Consensus includes gb:AL359338.1 /DEF=Homo sapiens mRNA full length insert cDNA cione EUROIMAGE. 2000 / 1.  //FEA=mRNA /DB_XREF=gi:8574097 /UG=Hs.50794 Homo sapiens mRNA full length insert cDNA clone EUROIMAGE.  2068071aaagtctagtgggatttataggaagctactattaggggctgtttggggaactggaagtggaagtcaagtggaaggaa	aactogagtcctaggaagagagagagagagagacaccaagaggcaccacagggtcoccagggtgaccacagagggaccacagaggcaccatgagacctgatactgagacatgagaattcacatcagagaacactggagacactgagacactgagacactgagacactgagacactgagacactgagacactgagacactgagacactgagacactgagacactgagacactgagacactgagacactgagacactgagagaacactgagagaacactgagacactgagagaacactgagagaacactgagagaacactgagagaacactgagagaacactgagagaacactgagagaacactgagagaacactgagagaacactgactacactgaagagagag

WO 03/039443		PCT/EP02/12	2303
233589_x_at	233559_s_at		
gb/AK000392.1	gb AK023415.1		
Consensus includes gb:AK000392.1 / DEF=Homo sapiens CDNA / DB_XREF=gi:7020451 / UG=Hs. 169758 hypothetical protein / FLJ20245gcactgggcccagtgggcgtgggcggggcgcacactgggccgccgcggggcgcgcgc	catgctcgggaggcacttcttcactgogctcggottcgtgtcgaatatgacttcggaggcactattcactgagggcactattcaggaggtactcattcaggaggcactattcaggaggtactattcaggaggtactattcaggaggtactattcaggagcatttcattca	Consensus includes gb:AK023415.1 /DEF=Homo sapiens cDNA FLJ1355 fts, clone OVAKO 1002162, weakly silling to BETA-TRCP (BETA-TRANSDUCIN REPEAT-CONTAINING PROTEIN). /FEA=mRNA /DB_XREF=gi:10435344 /UG=Hs.44743   KIAA1435   KIAA1435   proteingaggccgcagcagcagcagcgcgcgcaacatggcggccgaaatccactccaggccgcagagccgccggtgctgctgagcaagatcgagggggcaccaggacgcgcgcg	caacacagacccctaccagctgatgaatgcagtgaacacactggacagggatgtcctcaaccagctacacgtacagctcatggagctgaggagctgcaagggttacaagcagt gtaaccaccaggactccaggactgcaagggattacaagcagttacaagcagt gtaacccccggactcgaaacacatggacctgggaattccgtctcattt gtaacccccggactcgaaacactgcatgagaacacttccgtgagaacttacacctgaaaccatgttgactaaagatgaccccatcctcgctg

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233813 at	233613 x at	
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Consensus includes gb:AKU259U0; 1/DEF=Inclind sepiens cDNA: FLJ2347 fis, clone COLORA (COLO3425tttgaaaggttacctgagacctgtaccagecoggtgataccgcctttatttgtttttacagactttaatgttttacagacctaaatatgcacagatacattcttcttg COLO3425tttgaaaggttaccctgagacctgtaccagecoggtgataacgccctttttttttttttaaaaagtttttacagactttaatgtttttcattca	Consensus includes gb:AU156209 /FEA=ES1 /DB_XREF=gi:T1017 / 30 /DB_XREF-est-XO 150209 /FEA=ES1	

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gb AK022692.1	gb AK001782.1	gb AF090925.1
Consensus includes gb:AK022692.1 //DET=Horito sapiens control to the control to t	Consensus includes gb:AK001782.1/DET=Homo Sapiens CDNA FLA 1022 ns, Consensus includes gb:AK001836. /FEA=mRNA	Consensus includes gb:AF090925.1 //DEF=Homo sapiens clone HQ0452 PRO0452 mRNA, partial cds. /FEA=mRNA //PROD=PRO0452 /DB_XREF=gi:6690216 /UG=Hs.283921 Homo sapiens clone HQ0452 PRO0452 mRNA, partial cds. /FEA=mRNA, partial cds. /FEA=mRNA partial

wo	03/039443		PCT/EP02/12303
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234362_s_at	234140 s at	
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WO 03/039443	
234643 x at qb AK025451.1	
Consensus includes gb:Aku2-49 1. I/DET-FIVING Septems CDNA: 12.171981 is, clone Includes gb:Aku2-49 1. I/DET-FIVING Septems CDNA: 12.171981 is, clone Includes gb:Aku2-49 1. I/DET-FIVING Septems CDNA: 12.171981 is, clone Includes gb:Aku2-49 1. I/DET-FIVING Septems CDNA: 12.171981 is, clone Includes gb:Aku2-49 1. I/DET-FIVING Septems CDNA: 12.171981 is, clone Includes gb:Aku2-49 1. I/DET-FIVING Septems CDNA: 12.171981 is, clone Includes gb:Aku2-49 1. I/DET-FIVING Septems CDNA: 12.171981 is, clone Includes gb:Aku2-49 1. I/DET-FIVING Septems CDNA: 12.171981 is, clone Includes gb:Aku2-49 1. I/DET-FIVING Septems CDNA: 12.171981 is, clone Includes gb:Aku2-49 1. I/DET-FIVING Septems CDNA: 12.171981 is, clone Includes gb:Aku2-49 1. I/DET-FIVING Septems CDNA: 12.171981 is, clone Includes gb:Aku2-49 1. I/DET-FIVING Septems CDNA: 12.171981 is, clone Includes gb:Aku2-49 1. I/DET-FIVING Septems CDNA: 12.171981 is, clone Includes gb:Aku2-49 1. I/DET-FIVING Septems CDNA: 12.171981 is, clone Includes gb:Aku2-49 1. I/DET-FIVING Septems Gb:Aku2-49 1. I/DET-FIVING Septe	In ggcgggggttcgcagcgtccgtggactatttccctagcgaggactctaccgctgcggctactgcaagaacggtcgggcagctccaatggcatgtgggcaacactatggcatgtgggcaacacatatggcatgtggcaagaagtggaattactaggactgagattactcatagaacggaagttggaaaaaaatagtgtcgaagaagttgaaaattacggtgcgaagaagttacacaataagggccgaacttacacaatgggaagttgtagaagaattcacaaagaaggtttgaaaaaaatagtgtcgaaattacagggtcgaaattacaggaagttggaattacacaataagggacgaattactcaaggaagttggaattacacaataagggacgaaaaaattacaaaggaagttggaattacaaaataagggacgaaaaaattcaaaaaataggtgccaatggaagaagaaggaag

<b>WO</b> 03/0	139443	PC	Г/ЕР02/12303
234725 s at 234726 s at	1	234682_at	234660_s_at
gb AKU26133.1 gb AK025482.1		gb AL079341	gb AL080158.1
	Consensus includes gb:AK026133.1 /DEF=Homo sapiens cDNA: FLX2480 fts, clone HKC 1084 i. /FEA=IIINNA /DB_XREF=gi:10438886 /UG=Hs:9598 hypothetical protein from EUROIMAGE  /BB_XREF=gi:10438886 /UG=Hs:9598 hypothetical protein from EUROIMAGE  1955967cccgcatctgcaagggcgatgaggggggggggggggggg		aagaggaaatggggttctttatagaatgtggatttttcctacaagagactttgcagggcaatttcaaggtatggcaaggaaatatattttttgggtaaaacattttgattttcttcttgttatgcca gagtctgattggaaagtaagtcttgatatacagggttaaataaa

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235023_at	234862 at	234839_at	234764_x_at	
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Consensus includes gb:AA828371 /FEA=EST /DB_XREF=gi:2901470 /DB_XREF=est:0bb0g12.51 /CEONE=iiw/AGE:1555617	Consensus includes gb:AL0967707/DEF=Human DNA sequence from clotie RF 11-1906 of Children Consensus includes gb:AL0967707/DEF=Human DNA sequence from clotie RF 11-1906 (DEADH (Asp-Glu-Alagenes for novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor like) proteins, a DDX6 (DEADH (Asp-Glu-Ala-AspHis) box polypeptide 6 (RNA helicase, 54kD)) ps /FEA=CDS_3 /DB_XREF=gi:10198644 /UG=Hs.272282 Human DNA AspHis) box polypeptide 6 (RNA helicase, 54kD)) family) (olfactory receptor like) proteins, a DDX6 (DEADH (Asp-Glu-Ala-AspHis) box polypeptide 6 (RNA helicase, 54kD)) pseudogenetgtgctcacatttgctggtggtctcccttctacttcacacattgagaaacaaggatgtgaaagctgcctcaggctactcaggattttggattaagacaagatga gggcattgtcacacaccctcaaccccattcatctacacattgagaaacaaggatgtgaaagctgccctgagaaggtcactgaagggttttggattaagacaagatga gggcattgtcacacaccccaccc	Consensus includes gb:AL049277.1 /DEF=Homo sapiens mRNA	Consensus includes gb:U96394.1/DEF=Human affilt-streptococcalanti-myosin immunoglobulinlambda light chain variable region mRNA, partial cds. /FEA=mRNA /PROD=anti-streptococcalanti-myosin immunoglobulin lambda light chain region /DB_XREF=gi:2352087 /UG=Hs.307341 Human anti-streptococcalanti-myosin immunoglobulin lambda light chain variable region mRNA, partial variable region mRNA, partial cds:cdscagcccccagcgtctgggaccccccagcgtctgggaccccccgggcaggggaccaggggaccaggtaattatgtatactggtaccagcccdccagctctcagcgcccccagggaccagggaccagggaccagggaccagggaccagggaccagggaccagggaccagggaccagggaccagggaccagggaccagggaccagggaccagggaccagggaccagggaccaggggaccagggaccagggaccagggaccaggggaccaggggaccaggggaccaggggaccaggggaccaagctgaccggccatcagtgggaccatcagtgggatgagggaccagggaggg	agicaggotigccgcctcctightictcagicgcagictgaagcctigtctigctctcctccttittiggittiggittiggaactgactcgagiggiggagagitcgaatggcagittigtaaattagccatttaaaaaaaaacaatctgccatigtgattitigtaaagaagaagaagatcacaaaatttcacaaaagactgaaaaaagactgaaataagaagatgaaaataagaagatgaaataagaaga

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Consensus includes gb:BF-51633/ /FEX=EST, Weakly similar to unknown  //CLONE=IMAGE:3084166 /UG=Hs.115772 ESTs, Weakly similar to unknown  D.melanogasteragagytigctigctaaacatoctacccatgcatgygacagcatgitccaacaggaatcatccagccacatgycaacaggitcttgaggattatacttaaaaggattctggtgtcaacaatgtgaaaaagttttttaaaccttggtcatgggaataataattggagaattattttgggaatatatacttaaaaggaatatattgggcacaatgttttttaaacctggaatgaat	Consensus includes gb:AI076335 /FEA=EST /DB_XREF=gl:340513 /DB_XREF=est-0204a05X1 /CEONE=INFORMER /DB_XREF=gl:340513 /DB_XREF=est-0204a05X1 /CEONE=INFORMER /CEONE=INFORMER /DB_XREF=est-0204a05X1 /CEONE=INFORMER /CEONE	Consensus includes gb:AA677057 /FEA=ES17/DB_XREF=gl:26575797/DB_AREF=est.2704a05 v1.5170 CONSENSUS includes gb:AA677057 /FEA=ES17/DB_XREF=gl:26575797/DB_AREF=est.2704a05 v1.5170 CONSENSUS includes gb:AA677057 /FEA=ES17/DB_XREF=gl:26575797/DB_AREF=est.2704a05 v1.5170 CONSENSUS includes gb:AA677057 /FEA=ES17/DB_XREF=gl:2657579	tgtacctggcccacagctacctcccctgcagccctgagtcctgcttgtgtgcccggctcaggctgagactgcagtgcttgtccattcaccatganagaaagaagaagaagaagaaggaaggaaggaagga

wo	03/039443			PCT/EP02/12303	
236301_at	236293_at	236280_at	236265_at	236248_x_at	
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Consensus includes gb:AA789123 /FEA=EST /DB_XREF=gi:2849243 /DB_XREF=est:aa66f03.s1 /CLONE=IMAGE:825917 //UG=Hs.46645	Consensus includes gb:BE676335 /FEA=EST /DB_XREF=gi:10036876 /DB_XREF=est:7f27d12.x1 /CLONE=IMAGE:3295895 //UG=Hs.283313  ESTsgactgtggaatagtggtttctaaagctggctggacagcaaaccacctggggggagcttttaagaaactgaaattccatgtctcataccccagccctcacgtgaggtccaggaatctgtgtgttaaaaaataccaagccgccaaaacaacttggaaagtggtcgttttgcaggtggggggttttaagaaactgaaattccatgtctcataccccaggacccggaaaccgtaa gttgaantaagtgctgaaatgaggcaaatngatctactctctatntgtgattaatatcttcacaagcaagtattttcctttgtttg	Consensus includes gb:AI225238 /FEA=EST /DB_XREF=gi:3807951 /DB_XREF=est:qx12c04.x1 /CLONE=IMAGE:2001126 /UG=Hs.176920  EST stggttgttgtttcagcaccattttaaagaatttgaatacaaacaa	Consensus includes gb:BF438799 /FEA=EST /DB_XREF=gi:11451316 /DB_XREF=est:nab54b05.x1 /CLONE=IMAGE:3269696 /UG=Hs.88013 EST-sglottgtttaatggcattlcactgtttcattcctttaccaccgttataaaanttttctttattgtaattancagtgcnaagctatgtatttantcatggtaaaactcagtgtaaaatggtgtaatctaggaaaa agttaatttgtcaacttagttagttaggtttgtgtgtgtg	Consensus includes gb:Al859834 /FEA=EST /DB_XREF=gi:5513439 /DB_XREF=est:wm21a08.x1 /CLONE=IMAGE:2436566 /UG=Hs.155512 ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMILY SC SEQUENCE CONTAMINATION WARNING ENTRY  H.sapienstgggaggccaaggcgggctgatcacgaggtcaagagatcgagaccatcctggccaacatggtgaaaccctgtctctactaaaaatacaaaatacaaaatatagctgggtggg	gatgtcaaataatatttctcaatttgagaatttttactttagaaatgttcatgttagtgcttgggtcttaagggtccataggataaatgattaaaatttctctcagaaactta

WU	3/039443			PCT/EP02/12303
236535 at	236458_at	236378_at	236341_at	·
abIAW069285	gb BE875072	gb BF681360	gb Al733018	
Consensus includes gb.Avvoozeo in Ex. Eo. E.E. (UG=Hs.159452) /UG=Hs.159452 ESTsgactcatcctaatgaggggtgtaaaaaagtgtgctgcttcagaatgacgaaatatagttattgtaaaaaatgatatttatt	Consensus includes gb:BE8/30/2/FEA-E3/202 /CLONE=IMAGE:3888275 /UG=Hs.9002 /CLONE=IMAGE:3888275 /UG=Hs.9002 EST staaaactccggaattcttccccctctttgctgtctcatcctttaccttctggatttaggtgcttttaattccagttcaggaagataggaagataggaagattcttccaaaacatcacttttcctctgaagactgcttcttgtttgt	Consensus includes gb:BF681360 /FEA=ES1 / DB_XNE1 = 91.1750200 / CLONE=IMAGE:4297261 /UG=Hs.231898 ESTs, Weakly similar to A Chain A, Homology-Based Model Of Calcium-Saturated /CLONE=IMAGE:4297261 /UG=Hs.231898 ESTs, Weakly similar to A Chain A, Homology-Based Model Of Calcium-Saturated /CLONE=IMAGE:4297261 /UG=Hs.231898 ESTs, Weakly similar to A Chain A, Homology-Based Model Of Calcium-Saturated //CLONE=IMAGE:4297261 /UG=Hs.231898 ESTs, Weakly similar to A Chain A, Homology-Based Model Of Calcium-Saturated //CLONE=IMAGE:4297261 /UG=Hs.231898 ESTs, Weakly similar to A Chain A, Homology-Based Model Of Calcium-Saturated //CLONE=IMAGE:4297261 /UG=Hs.231898 ESTs, Homology-Based Model Of Calcium-Saturated //CLONE=IMAGE:4297261 /UG=Hs.231898 /UG=Hs.231899 /UG=Hs.23189	Consensus includes gb:Al733018 /FEA=ES1 //B_XREF=9l.5054 IS1 //B_XREF=9l	ESTstttaacttttttttttttttttttttttttgagaccctgtccaaacaaa

<b>WO</b> 03/0	39443			PCT	/EP02/12303
236707_at	236656_s_at	236648_at	236606_at	236557_at	
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WO 03/039443				PCT/	EP02/12303
236854 at	236837 x_at	236796_at	236787_at	236728_at	
gb AA743694	gb BE669806	gb Al052447	gb AW591809	gb AW070437	
Consensus includes gb:AA743694 /FEA=EST /DB_XREF=gi:2/84510 /DB_XREF=est:ny92d0 /.S1 /CLONE=IWAGE:1285 /41 //UG=Hs.48984  ESTsggaaaagtccctcaaaaatttgtttttccccaatttaaaaagaaag	Consensus includes gb:BE669806 /FEA=EST /DB_XREF=gi:10030347 /DB_XREF=est:7e25b04.x1 /CLONE=IMAGE:32834 / 7 /UG=Hs.129137  /UG=Hs.129137  EST stotcattttgaaaacttnaaaaaaaaaaaaaaaaaaaaaattttgtagttotongggtaaaaaaaaaa	Consensus includes gb:Al052447 /FEA=EST /DB_XREF=gi:3308438 /DB_XREF=est:oz07g04.x1 /CLONE=IMAGE:1674678 /UG=Hs.118659 ESTsgcgtggtgccaccgcagactaaaagcagatataagtcaagtgctactgacttaagtttggcaaaatcactcctcacagcccgctctgttttagaaatgtttatatttctgatatcacttttgttaatttgaagaacttttaaaataccatcattgtttcaaaaccaaaatgtggaaggtgtggatcaccttcctgaatttacagaaaagtttttgggtacatttttgggaagattgttcacggcaggatgtggtgcccgtgncttgcggatcacgttgtcgtacactgactgacttaaacttagagtctttgaaaaatgcccattggtaagtcacattgtttccctgaaggtgtggtccaggaagaagatgtcccgtgncttgcggatcacgttgtctgtacactgactgacataccaacttagagtctttgaaaaatgcccattggtaagtcaacattgtttccctgaaggtcctnagacagaaaaa	Consensus includes gb:AW591809 /FEA=EST /DB_XREF=gi:7278974 /DB_XREF=est:xx85d08.x1 /CLONE=IMAGE:2850447 /UG=Hs. 126630 ESTsagtgcaagggctcccctgtcgccgatgtgttctttgaagcagatgctgtgcctgatacctgctgagaggtcccaccgcctttgagcttctgggtcgagagaggtccaagttgcacccttctgaggccaagttgccaccttctgaggccttctgggtcaaggccaagttgccaccttccctgctgaggagactgccatgcaccccatgtgttctccccttccctgatacccccatgtgttctccccttccctgatactcaagccccttgaggagtttctaggccacaaaataattcttcctagaacaactccacgtgtgttatcgcccttgcagctggggtggccaccactggggagaggagggggggg	Consensus includes gb:AW070437 /FEA=EST /DB_XREF=gi:6025435 /DB_XREF=est:xa11b11.x1 /CLONE=IMAGE:2567997 /UG=Hs.26330 ESTsgaactactgattatattctcccttctcctaatgtagaatgctttattctactgccatctttctgtctg	atcacatataggactacagtatcattattacaactgaagaaattaatgttaattctataatatcaactgagaatgggtgtcttttaaaatttgnatagacatgccctgtgagctagcagagcttttatttttctcatatatccaaaaatcaggaggcaagcagctatggtgacaaggtcaggtccaggtccagggtctctactgttctcctggccttttctcatgctggctacttcaggatttgagtgtctactactttttttt

wo	03/039443			PC	CT/EP02/12303
237068 at	237006_at	236979_at	236914 at	236908_at	236892_s_at
gb Al871655	gb AA703523	gb Al821801	gb AW080028	gb BE550429	gb BF590528
Consensus includes gb:Al871655	Consensus includes gb:AA703523 /FEA=EST /DB_XREF=gi:2/13441 /DB_XREF=est:2/12n12.51 /CLONE=IM/AGE-430115 /DG=Hs.24128 /UG=Hs.24128 /UG=	Consensus includes gb:AI821801 /FEA=EST /DB_XREF=gi:5440880 /DB_XREF=est:nr06c07.x5 /CLONE=IMAGE:T161036 /UG=Hs.168974 ESTs, Highly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY  H.sapienscctttctgagcagctgtgtttgaagaagctagtgggaaaagttccaggattccaggattccaggaactaccaagaggtagaaacatttgttgatttaccagtgttttaacttccttgctgggctgaaaacttgttgggaaaacttgacaggaactactactactactactacttggggacttctttgaggcacaaacggaattgcaggaacctctactactactattgtgggaacaacggaattgttggaacactctactcattggggacttctttgaggaacacattgggaacactttttgaggaacacattggggaacacattggggattggggttggattcaggaggtttttggggaacacattggggattcaggaggctttttggggattcaggaagactttttgaggagacctggttgggaacactggggttggggtgttttggggttgggtatcattggggaacactgggggttgggaacactgggggttggggaacactgggggttggggaacactgggggttggggaacactgggggttggggaacactgggggttggggaacacttcttggggaacactgggggttgggaacactgggggttggggaacacttcttggggaacacttcttgaggagaggtggggaacactgggggaacactgggggggtgggggggtatcacatggggaacattcatggggaacatcacttcctggggaacatcacttcctggggaacatcacttccttgttgggaacatcattggggaacatcagggggggg	Consensus includes gb:AW080028 /FEA=EST /DB_XREF=gi:6035180 /DB_XREF=est:xe11g09.x1 /CLONE=IWAGE:2000040 /UG=Hs. 131601 ESTsacaggctttcttagttgagctgtcttcctgaggttgttttggagccgctgcgtncatggataaataactccctaaagccagtcccaacaagcttgcactgaacatcaagaagcctgacatcaagaagcctgaacatcaagaagcctgaacatcaagaagcctgaacatcaaagtccttcaaatgcaagaagcccaacaagttgctggtcttttaatcaacagacaactgggcaggca	Consensus includes gb:BE550429 /FEA=EST /DB_XREF=gi:9792121 /DB_XREF=est:7a25b09.x1 /CLONE=IMAGE:3219737 //UG=Hs.143905 //UG=Hs.143905 ESTstttataaaacacccagaacagtacctggcacatagtaatcactacgtatgtgtttgtt	Consensus includes gb:BF590528 /FEA=EST /DB_XREF=gi:11682852 /DB_XREF=est:7h36h10.x1 /CLONE=IMAGE:3318115 //UG=Hs.269918 EST sgacaggggccaatattcaaacgctgcagcagaggcgcatagcctagccctggccaccccctcttgggaaggaggtcgagttaagccggttggaggttggaggtccaaccaggaa cggaaattacgacggtgtggttccttaaggatttggccccagtccactaccaaatttttcccaaatcatatttaggtagacttcgcttgaaaagatcgagaatggagggggggg

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WO 03/03	9443			PCT/EP02/12303
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Consensus includes gb:AW291535 /FEA=EST /DB_XREF=gl:bb9817 17/DB_XREF=est.OFFI-DE-agr-P-12-0F018 1/ 1/CLONE=IMAGE:2724454 /UG=Hs.254980   /CLONE=IMAGE:2724454 /UG=Hs.254980   EST-sccagtattctcccaaggatgtgagttctgagttcacattatttaggttaaatctttacttcacatagttctcatttatattttcacatttcacatttcacttcatgtgctgtgctcttatacttcactttcactttcactttcactttcacattgccataaatagcaagaatgatgatgtgtgtg	Consensus includes gb:AA669114 /FEA=EST /DB_XREF=gi:2630613 /DB_XREF=est:aa61n02.51 /CLONE=IN/AGE.02/3/3///UG=Hs.116665  EST sttaagtaaaaggcacaatggtactacagaattaaaatgtaggtctaacataatgccagttccactttgtttttgcatttgtattgaagaatgtatgt	Consensus includes gb:BF971873 /FEA=EST /DB_XREF=gi:12339088 /DB_XREF=est:602240462F7 /CLONE=IMAGE:4328990 /UG=Hs.25092 /CLONE=IMAGE:432890 /UG=Hs.25092 /CLONE=IMAGE:4328990 /UG=Hs.25092 /CLONE=IMAGE:432890 /UG=Hs.25092 /CLONE=IMAGE:432890 /UG=Hs.25092 /CLONE=IMAGE:432890 /UG=Hs.25092 /CLONE=IMAGE:432890 /UG=Hs.25092 /CLONE=IMAGE:432890 /UG=Hs.25092 /UG=	Consensus includes gb:Al125255 /FEA=EST /DB_XREF=gi:3593769 /DB_XREF=est:qd8/h09.x1 /CLONE=IMAGE:1/35013 /UG=Hs.269918  /UG=Hs.269918  ESTsgataattgaggaaaaaaaaaaaaaaaaaaaaaaaaaaa	Consensus includes gb:AW195920 /FEA=EST /DB_XREF=gi:6475150 /DB_XREF=est:xn86g08.x1 /CLONE=IMAGE:2701406 /UG=Hs.144252 ESTsaattgcacagccagctacttccagaatcgntggtccaaagaaatcacgacaggcgctaagtttggggcaatccatttaatgctactaagttgtgggttgtttgagcagccccagaatcacttccttgaggtcacacgctaaccaagctgtgattcgaacactgcctctcaaattcacgagcaaatcagggggaattctttttaattttaattttatgtataaatagttgtataataa	ESTsgatcccataatgcatttatataattcttgattcatctttgattataagtttttttgtgattataaattcgatagaggaaaaatcattatggtccatttaaacttgaagaaatgtatctctccattgagcattaaattgccatatccattntaggaaagtttaatttaa

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240239 at	240201_at	240113_at	240106 at	240061 at
gb N63953	gb Al821995	gb A 732466	gb Al633523	gb AVV664903
Consensus includes gb:N63953/FEA=EST/DB_XREF=gl:1702/DB_XREF=gl:7702/DB_XREF=gl:7702/DB_XREF=gl:7702/DB_XREF=gl:7702/DB_XREF=gl:7702/DB_XREF=gl:7702/DB_XREF=gl:7702/DB_XREF=gl:7702/DB_XREF=gl:7702/DB_XREF=gl:7702/DB_XREF=gl:7702/DB_XREF=gl:7702/DB_XREF=gl:7702/DB_XREF=gl:7702/DB_XREF=gl:7702/DB_XREF=gl:7708/DB_XREF=g	Consensus includes gb:Al821995 /FEA=EST /DB_XREF=gl:3441074 /DB_AREF-est-083107.30 /CEORE-INFACE-1820 /DB_XREF-gl:3441074 /DB_AREF-est-083107.30 /CEORE-INFACE-1820 /DB_XREF-gl:3441074 /DB_AREF-989421	Consensus includes gb:AI732466 /FEA=EST /DB_XREF=gi:5053579 /DB_XREF=est.zn87gvb.x57c.Consensus includes gb:AI732466 /FEA=EST /DB_XREF=gi:5053579 /DB_XREF=est.zn87gvb.x57c.Consensus includes gb:AI732466 /FEA=EST /DB_XREF=gi:5053579 /DB_XREF=est.zn87gvb.x57c.Consensus /CLONE=IMAGE:305210 /DD-XREF=IMAGE:305210 /DD-XREF=IMAGE:30521	Consensus includes gb:Al633523 /FEA=EST /DB_XREF=gi:4684853 /DB_XREF=est.flood F.XT /CLONE=IN/OSE.2 12000 //UG=Hs.44705 //UG=Hs.44705 ESTsaatcaggatgtgctggcgaattcctggctgataagttctgtgaccaagcatgcaatgcatgtctgtc	Consensus includes gb:AVV664903 /FEA=EST /DB_XREF=gi:7457447 /DB_XREF=est:hi85e04.x1 /CLONE=IMAGE:2979102 //UG=Hs.186649 //UG=

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240785_at	240740_at	240581_at	240572_s_at	240449 at
gb BE671136	gb AW182300	gb AW007727	gb BF436632	gb AW204518
//UG=Hs.243602 ESTsgcctaccaccatccttcgagatcatcaccaatgtccctgggctatcatggggatctgtgggggtctgacaatctcacaggaaaagtcctcagtactgtaaggctaccttgaaattatagcaaatccaagctaccacgggttagataaattaccaaggaaagtcctcagtaaggcacttggaaattggcaacttgaaagtcctcaggaagga	/UG=Hs.112612 /U	Consensus includes gb:AVV00 / /2 / FEA=EST /DB_\NEF=ni-6450760 /DB_\NEF=est:xi41a03.x1 /CLONE=IMAGE:2659756	Consensus includes gb:BF436632 /FEA=EST /DB_XREF=gi:11449031 /DB_XREF=est./puspuz.xi /CLONE=IMAGE:2512621	gaaaaattattctatgtctttaaaattgcctgctttgggtttactttacagatggtataagattgttgtctgttaaaaaattcatgcaactgtgtattttatggtcgactgacatattctgtcttaattccatag gaaaaattattctatgtctttaaaattgcctgctttgggtttactttacagatggtataagattagaataaagtttctcgattaattcaaaactgaaaaaaaa

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241395_at	241383 at	241370_at	241353 s at	240842_at
gb AL572553	gb H05959	gb AA278233	gb AW471181	gb AA853996
Consensus includes gb:AL5/2553/FEA=ESI/DB_XREF=gi:12930934/Db_XREF=est.AL5/2553/CEORE—Coolings (Consensus includes gb:AL5/2553/FEA=ESI/DB_XREF=gi:12930934/Db_XREF=est.AL5/2553/CEORE—Coolings (Coolings) (Coolin	Consensus includes gb:H05959 /FEA=EST /DB_XREF=gi:869511 /DB_XREF=est:yi/bqub.si /CLONE=IMAGE.444004 /UG=Hs.62189 /UG=Hs.62189 EST-sccaactcttggaggggggggggtgtgggtctccctcagactatggactcagctaacaccgaaccccccgcagagctcccaaagggaagagctttccctacagcttccactccaactctggactcagcttgggaggcgggggggg	Consensus includes gb:AA278233 /FEA=EST /DB_XREF=gi:1920173 /DB_XREF=est:zs / /a10.r1 /CLONE=IMAGE: /03482 //UG=Hs. 100691  EST-stgaagtgttgggattacaggcgtgcagctgcgcccggccaattttaacttttcataattagatttgtatatatttatt	Consensus includes gb:AW471181 /FEA=EST /DB_XREF=gi:7041287 /DB_XREF=est:xv13b04.x1 /CLONE=IMAGE:2812973 /UG=Hs. 160874  ESTsgaangncggggccgagggcggccctctgcggacttggagacccggnaggacgggacg	atattttgagataagaagttaagctctagtataacaatgatatgggtcaaagaaaaaaaa

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241734_at	241525_at	241483_at	241464 s_at	241421 at
gb Al391443	gb AV700191	gb AA156795	gb Al973033	gb N92599
Consensus includes gp:Al391443/FEA-E317/Pb_ANET-gi-76-20-20-20-20-20-20-20-20-20-20-20-20-20-	Consensus includes gb:AV700151 /FEA=EST /DB_XKEF=gl: 10302102/DB_XKEF=st-rf06e06 x 1 /CL ONF=IMAGE:2107138	Consensus includes gb:AA156795 /FEA=EST /DB_XKEF=gi:1/28410 /DB_XKEF=est.2/2003.51 /CEOKE=INFOCE.302.51 /UB=HS.62772 /UG=Hs.62772 /UG=H	Consensus includes gb:Al973033 /FEA=EST /DB_XKEF=gl:5/69859 /DB_AKEF=est.Wi4eg03.XT/CECNEF=WAGE-EST-NO-LAXI /CECNEF=WAGE-EST-NO-LAXI /CECNEF=WAGE-	gcaacctccgcctcccaggctcaagcaattctcgtgcctcagcctcccaagtagctgggatcacaggcacgcac

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241930_x_at	241810_at	241795_at	241754 at	241742 at
gb AA223204 gb AA150242	gb BF509144	gb]AA678073	gb AA829836	gb AW027174
Consensus includes gb:AA223204 /FEA=EST /DB_XNET=gi:10707072773778186898  [UG=Hs. 186898]  ESTstgaagcaaaagaacaaaanctcattcaggataattggttattctaaaatacagtcatttctaaaattatgaagtgttcaggacctttgggagtgaaagaattgggaatccaggggaaggtgaaggaag	Consensus includes gb:BF509144 /FEA=ES1 /Db_\NEF-91.1752772 /DB_\NET-91.1752772 /DB_\NET-91.1752775 /DB_\NET-91.1752775275 /DB_\NET-91.1752775 /DB_\NET-91.1752775 /DB_\NET-91.17527755 /DB_\NET-91.1752775 /DB_\NET-91.1752775 /DB_\NET-91.1752775 /D	Consensus includes gb:AA678073 /FEA=EST /DB_XREF=gi:Zboospo /DB_AREF=est-21129129 /DB_AREF=est-21129129 /DB_AREF=est-21129129 /DB_AREF=est-21129129 /DB_AREF=est-21129129 /DB_AREF=est-21129129 /DB_AREF=est-21129129 /DB_AREF=est-111-H-BI4-aov-a-05-0-UL.s1	Consensus includes gb:AA829836 /FEA=ES1 /DB_ANEF-91.29233 /DB_ANEF	gaagttgtaagatgactcactgaggaagggactgctttatacatcacagtactgctatttaaaaggaacacagaaattttaaaacagaaattttaaaacagaagttgtaagatgactcactgaggaagggactgctttatacatcacagtactgctatttaaaaggaacacagaaattttaaaacagaaatttqctacagb:AV027174 /FEA=EST /DB_XREF=gi:5885930 /DB_XREF=est:wt72c10.x1 /CLONE=IMAGE:2513010 /DG=Hs.239276 ESTs, Weakly similar to FYB_HUMAN FYN-BINDING PROTEIN /UG=Hs.239276 ESTs, Weakly similar to FYB_HUMAN FYN-BINDING PROTEIN /UG=Hs.239276 ESTs, Weakly similar to FYB_HUMAN FYN-BINDING PROTEIN /UG=Hs.239276 ESTs, Weakly similar to FYB_HUMAN FYN-BINDING PROTEIN (Greanatttnaaggganatcggtggttcacaggganatcggggnattcacaggggnanttccgnaanatttnaaggggnantcggtggttcacaggggnanttcggggnanttcggggnanttcggggnanttcgggggnanttcgggggnanttcgggggnaatcgggggggggg

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242292 at	242223_at	242104_at	242065 x_at	: 241985 at	241975_at
gb H12084	gb AA505323	gb AA826288	gb BG477984	gb Al814405	gbJN29850
Consensus includes gb:H12084 /FEA=EST /UB_AREF=gl.o/0904 /UB_AREF	Consensus includes gb.AA30332371 EATE Consensus includes gb.AA3032371 EATE Consensus gb.AA3032371 EATE	Consensus includes gb:AA826288 /FEA=EST /DB_ANET = 91.2000000000000000000000000000000000000	Consensus includes gb:BG4 / /984 / FEA=ES1 / DB_/NEI-gi: 1970-2070-2070-2070-2070-2070-2070-2070-2	Consensus includes gb:Al814400 /FEA-EST /DB_ARE 91.012-91.	gttettetgtteteattetttteacteegataaagagaactgetettttteetattteetattteetageaegatgtagatgaagaagtgaagtgaagtgaagtgaatgeattatttteetattteetettetteetettetteetetteetetteetetteetet

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242414_at	242404 at	242388_x_at	242363_at	242329_at
gb AW960707	gb AW518888	gb AVV576600	gb BF592008	gb AW071804
Consensus includes gb:AW960707 /FEA=EST /DB_XREF=gi:8150391 /DB_XREF=est:EST372778 /UG=Hs.148324 ESTsganggtgccactgcactccagcctgggtgatagaggcgaggactctgtctccaaaagaaag	Consensus includes gb:AW518888 /FEA=EST /DB_XREF=gi:7156970 /DB_XREF=est:ha45g06.x1 /CLONE=IMAGE:28 / 6698 /UG=Hs.40937  ESTscacatgctgcaacatggatganccttgaaaatattgtgccagggaaagaagccagaggcaaagngccncatgttgtagggattccatgatatgaaaggncctaataagcaaaaccactggacttgaaaatattgtgccaggggaaagaagccagagggcaaagngccncatgttgtagggattccatgatatgaaaggncctaataagcaaaaccactggactgaattggggtgaatnntttggtatatgaattacgtgtaaaaactgtaaaaactggaaaaaaaa	Consensus includes gb:AW576600 /FEA=EST /DB_XREF=gi:7248139 /DB_XREF=est:UI-HF-BR0p-ajy-c-07-0-UI.s1 /CLONE=IMAGE:3076212 /UG=Hs.123581 EST sgaaatccactaagaaatcattcactattggttcactcaacaagcatttattaaatatatat	Consensus includes gb:BF592008 /FEA=EST /DB_XREF=gi:11684332 /DB_XREF=est:7o35e09.x1 /CLONE=IMAGE:3576280 /UG=Hs.87372 EST scagcattgtctacaagtccgaaagtacggtgacaaatatctaagaatcagtattgaaatcagtnaatttcaggaaattgatcaggaaatggacattgatcagatcttgatttattattgatcccaaaccttttgtactntctgaagtgtaactgtcttttattcaacagaactgaact	/UG=Hs.31110 ESTs, Weakly similar to MAGE-B4 H.sapiensacttaagttgaacatcctaggtctatgaatgacgttggtcaaatgttttattgttctctgttttcggtttttagcaggagagatttgctgttcataaaagaaattgggagagagtatatcatttattgcctgtaacttattatagcattggaataagctgttctttggaggtttgagagactttaccagtaccagtacatcattcccccccc

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242520 s at	242463_x_at	242458_at	242448_at	242434_at	
gb AW511110	gb Al620827	gb AA721230	gb Al800895	gb AW771952	
Consensus includes gb:AW511110 /FEA=EST /DB_XREF=gi:/ 149188 /DB_XREF=est.1043000.x1 /CCORE=IMPORT.2912207 /UG=Hs.193754  ESTstttttagcaataaaaaaatgcatgtttatttgtaaattgtgcagagccattttaaaactttaaaacagattttgacatgcctatgctgaaataaaatcctccagccacataactctaag	Consensus includes gb:Al620827 /FEA=EST /DB_XREF=gi:4629953 /DB_XREF=est:tuboc (2x) /CEONE=IMAGE:2277942 /UG=Hs.116391 ESTs, Weakly similar to A32891 finger protein 1, placental /UG=Hs.116391 ESTs, Weakly similar to A32891 finger protein 1, placental /UG=Hs.116391 ESTs, Weakly similar to A32891 finger protein 1, placental /UG=Hs.116391 ESTs, Weakly similar to A32891 finger protein 1, placental /UG=Hs.116391 ESTs, Weakly similar to A32891 finger protein 1, placental /UG=Hs.116391 ESTs, Weakly similar to A32891 finger protein 1, placental /UG=Hs.116391 ESTs, Weakly similar to A32891 finger protein 1, placental /UG=Hs.116391 ESTs, Weakly similar to A32891 finger protein 1, placental /UG=Hs.116391 ESTs, Weakly similar to A32891 finger protein 1, placental /UG=Hs.116391 /UG=Hs.116	Consensus includes gb:AA721230 /FEA=EST /DB_XREF=gi:2737365 /DB_XREF=est.nz/2b04.s1 /CLONE=IMAGE:1309/5 /UG=Hs.102398 /UG=Hs.102398 EST stcttaaaaggtagtactgtaagggggaacattatttccggcagaaggtacaaaagtctgttgtttctatttgcaagacgctttttttt	Consensus includes gb:Al800895 /FEA=EST /DB_XREF=gi:5366367 /DB_XREF=est:wg14b02.x1 /CLONE=IMAGE:2365035 /UG=Hs.131929 ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY  H.sapienstttgttttatttaagctgcattaactccaatgtatatgaaaggggcatttttataattgtaaagttataatgtaaaacttttcctaatgtaaagttagtcaatgagtgttttattaacagggtgttcacaatgaatagtcgtcattgttcagtgttcacaatgattaaattctgtgtcattgttagctgttcacagtgttgatcacaaaggacaaaaggaggttgaaaaacgttttgatcacaaaggacaaattctgaacaattctgtaacaattgttaaaattctgtgtcattgttagctgtcacaggaggagaaaaaaaa	Consensus includes gb:AW771952 /FEA=EST /DB_XREF=gi:7704001 /DB_XREF=est:hn66h01.x1 /CLONE=IMAGE:3032881 /UG=Hs.191581 ESTsgtggtagctattttaaatgtcttatttttcctcaagatagtcccagcatttacaacgttatgtatcccccttaaagaaacacgcacaaaaaatgaaaagcttaggatccagtctaccacttgcttttttcagtgttttttcagtgtctttggagatggctttattagcctgtaagatctacctcattttttcactgctttgtgatatccattgtatgaatgtaccataattcatacagtcccctgttgatgggcctctataggttcttttctgccttttgctattacaacagtactgtgccaaatatccccgcacactgtcctggataaattgatgaaattgaaattgatgggtgcatttgtatttgatagaaattggaaattggaaattgtagtgtgtgtgtgtgtgtgtgtatgaaaatgttcatcctgaaactatgaaactgtgtgtg	gtgagtgcacagnagatggaggtttgctgggcagagacactgggctggcctagacactgcctttggtgataccctaaaccaaaggggccagtcccacagtaagaaggagacca ctactactcctgctgccctcctcccccccccc

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242729_at	242695_at	242633 × at	242541_at	242525_at	
gb BE551384	gb BF512254	gb AA829635	gb AV692159	gb AA747436	
Consensus includes gb:BE551384 /FEA=EST /DB_XREF=gi:9793076 /DB_XREF=est:7b64a09.x1 /CLONE=IMAGE:3232984 //UG=Hs.166999 ESTs, Moderately similar to I38344 titin, cardiac muscle	Consensus includes gb:BF512254 /FEA=EST /DB_XREF=gi:11597433 /DB_XREF=est:UI-H-BW1-amb-a-09-0-UI.s1 //CLONE=IMAGE:3069209 /UG=Hs.126767 /CLONE=IMAGE:3069209 /UG=Hs.126767 ESTscggataccattttcacacaggaaacagttatgacatgattacgattttaaacgactcactatagggaatttggccctcgaggccaaaattcgggcaaaagggtgcaactttctncagttattgagtatgttatacaaggcatgggaaaggggaaaggggcaaaggggcatttttaacttaaaggaatcattaaaggaatcattatgtggattaatgaatcactttttgcctttgtatcagtcatcccttgtatcagtggataccacagatgttcaaattccttatgtaaaatattgtagtatttgcatataaccacacaca	Consensus includes gb:AA829635 /FEA=EST /DB_XREF=gi:2902734 /DB_XREF=est:od35a09.s1 /CLONE=IMAGE:1369912 /UG=Hs.186589 ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY  H.sapiensccacagaaagttcacagntttcagagattgtggtagatacttccctggccttagagaaagagagttgcttttgccctctttggagccagggtgaattgagtgttggggctcacacctgtaattctcagcactttagg aggctgaggctggggctggggctgagcactttaggacctttaggaacaggataaaaggtaagagtcagggggggg	Consensus includes gb:AV692159 /FEA=EST /DB_XREF=gi:10294022 /DB_XREF=est:AV692159 /CLONE=GKCAOB12 /UG=Hs.301496  ESTstgcatttgaaactnatgcaataattatnctnagnngtatttcttacagtgagacaacaggcgatgtcagtgagggcgatcatagggcataagcctaagccataccatgcagcctttgtgccagcaaccaaatcccatgtttcctactgtgttaagtttaaaattgcatttattatgaattgtctacatttctgaggagatgtcatgggagaatgcttaattttcttctctgaacttcaaaat attaaaatattttcttttttttgattaaagtataaagtaaaattgacctatggatgaggtcaattggaggagatgctattggttttataaattacctttttataattcactggttttctgtcattnttcagagtttagattggagtccatgtttgtctgttgtggagacaagtattgaattgaaattgaattgaaattgaaattgaaattgaaat	Consensus includes gb:AA747436 /FEA=EST /DB_XREF=gi:2787394 /DB_XREF=est:nx88f10.s1 /CLONE=IMAGE:1269355 //UG=Hs.163105 ESTsatgtcttctcatagatggttggcagggctggtcgccgggagagaga	gtaaacaagacagtgatgcaacatgagaaccaggcctcaattttgctttggttgaacaggcttggttgaagagcttttaatcctattcatattatatatcttgagtggggattttttcataaat cccttccaatttannnnnnnnnnnn

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Cluster Incl. AW001443:wu31e12.x1 nollio sapiens color, 3 end colore in the color of the color o	Cluster Incl. A1524 i 36 in 0 solver is control of the control of	Cluster Incl. W22625:71E5 Homo sapiens cDNA /clone=(not-directional) /gb=W22625/gl=12990/ /uy=15.2-109/ /len=632ctgggaatgaataaagcacttacagaagagtatcctaatgaaaacactttaaaacagattggaaaacatgagcacttacagaagagtatcctaatgaaaacacatttaaaacagattgggaaaaactgggaaggtgtttattacatgaagagatgcatttattcctaatgaaaaacacatttaaaacagattggaagatgcatttattcctaatgaaaacacattataaacagatttattacattgtcagatttattccattttcctgctggtgtttattcctaaactggtgattattcctaattcctaattcctgctggtgttcttgtgctgattggtgcatttattccacacagaattggattggattattccacacagaagcagcattaactccacacagaagcagcattaaacacacac	cagaaataaaggcgaagacccannnnnnnnnnnnnnnnnn

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n iii iii iii iii	59697_at	58780_s_at	57588_at	
ab L42374	gb AA582932	gb R42449	gb R62432	
Homo sapiens PP2A Bb6-beta micina, complete cdsccgtcgccctcctacggcagcccccaggaccccaggagttgcagctctaggttttcgagaaagccagggtgggaaccctaactggactcttcgggaccccaggaagga	gtatcaagacctatgo ccagtnnnnnnnr aaacatggaatcag staaacttttggtggco nnnnnnnnnctcci	Cluster Incl. R42449:yg02a07.s1 Homo sapiens culva, a end /cluster Incl. R42449:yg02a07.s1 Homo sapiens cultation cultatio	Cluster Incl. R62432:yg52e11.s1 Homo sapiens cDNA, 3' end /clone=IMAGE-36023 /clone_end=3' /gb=no2432 /gl=no2432 /gl=no24324 /gl=no2432 /gl=no24324 /gl=no2	/gi=5393194 /ug=Hs.109778 // lig=Hs.109778 // lig=Hs.109778 // lig=S57atcccattgccctcccctaacttgtgtgtgnccctgccctcccacccataacagggcactaggccggggaggcagggaaccgtttttcccttttcctacatcttccacaggttc // lig=557atcccattgccctcccctaacttgtgtgtgnccctgccctcccacccataacaggccactaggccggggaggcagggaaccgtttttcccttttctcacatcttccacaggttc ggctngggncccgnctnnannngcctaaggccannnnnnnnnn

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77508_r_at 90610_at	.][.	74694 s at	64942 at	
gb AW001436 gb Al654857		abiAA907940	gb Al937160	
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#### Claims

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- 1. A method of determining whether a patient sample contains leukemia cells or other cells comprising the steps of
  - a) determining the the expression profile of a group of markers in a patient sample
- 10 and
  - b) concluding from expression profile whether the patient sample contains leukemia cells or other cells

characterized in

that the group of markers consists of markers selected independently from the
markers listed in one or more of the tables 3 to 6, tables 15 to 20, tables 29, 30, 41,
or 42 and whereby the number of markers in the group is between one and the
total number of markers listed in the tables 3 to 6, tables 15 to 20, and tables 29,
30, 41, or 42.

20 2. The method according to claim 1

characterized in that

the number of markers in the group is between two and the total number of markers listed in the tables tables 3 to 6, tables 15 to 20, and tables 29, 30, 41, or 42.

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3. The method according to claim 1 or 2

characterized in

that the group of markers consists of all markers listed in one or more tables, whereby the tables are selected from the tables 3 to 6, tables 15 to 20, and tables

30 29, 30, 41, or 42.

- 4. A method of determining whether a patient sample contains leukemia cells or other cells and at the same time or subsequently determining the type and subtype of leukemia cells, if leukemia cells are present, comprising the steps of
  - a) determining the expression profile of a group of markers in a patient sample and
- b) concluding from the expression profile whether the patient sample contains leukemia cells or other cells and at the same time or subsequently determining the type and subtype of leukemia cells, if leukemia cells are present, characterized in
- that the group of markers consists of markers selected independently from the
  markers listed in one or more of the tables 16 to 20 or table 29 or 30 and whereby
  the number of markers in the group is between one and the total number of
  markers listed in the tables 16 to 20 or table 29 or 30.
  - 5. The method according to claim 4
- the number of markers in the group is between two and the total number of markers listed in the tables 16 to 20 or table 29 or 30.
  - 6. The method according to claim 4 or 5
- 20 characterized in that the group of markers consists of all markers listed in one or more tables, whereby the tables are selected from the tables 16 to 20 or table 29 or 30.
  - 7. The method according to any of claims 4 to 6
- 25 characterized in that it is differentiated between four types of leukemia cells in the patient sample and that the other cells are normal cells.
- 8. The method according to any of claims 1 to 7
  30 characterized in that at least one marker is selected from the group consisting of
  ADCY3.
  - adenosine deaminase (ADA),

- ARGHGAP4,
- B-cell, a specific coactivator of octamer binding transcription factors,
- CAPN3, a member of the papain superfamily,
- *CBFB-MYH11*,
- 5 CD24,
  - CD27,
  - CD74,
  - connective tissue growth factor (CTGF),
  - CTGF,
- 10 CTSW,
  - MYH11
  - glucocorticoid receptor beta
  - CBFA2T1 (formerly ETO)
  - HLA-DMB
- 15 HOXA9
  - HOXB5
  - IRF4, an immune system-restricted interferon regulatory factor
  - KIAA1013
  - LCN2, a modulator of inflammation
- 20 LEF-1
  - MBNL
  - MSF translocation partner of the mixed-lineage leukemia gene (MLL) in AML
  - NCOA1,
  - OS-9
- 25 Phospholipidscramblase 1 (*PLSCR1*)
  - POU2AF1
  - POU2F2
  - POU4F1
  - SCYA3
- 30 DEFA3, SGP28, CAMP, CLC

- SOCS-2 and
- TRB and CD3D
- 9. A method of differentiating between two types of leukemia cells or one type of
- 5 leukemia cells and normal cells or non-leukemia in a patient sample comprising the steps of
  - a) determining the expression profile of a group of markers in the patient sample and
- b) concluding from the expression profile which type of leukemia cells the patient
   sample contains or whether it contains normal cells or non-leukemia
   characterized in

that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 3 to 6 or tables 7 to 12 and whereby the number of markers in the group is between one and the total number of markers listed in the tables 3 to 6 or tables 7 to 12.

- 10. The method according to claim 9
  characterized in that
  the number of markers in the group is between two and the total number of
  markers listed in one or more of the tables 3 to 6 or tables 7 to 12.
- 11. The method according to claim 9 or 10 characterized in that the group of markers consists of all markers listed in one or more of the tables 3 to 6 or tables 7 to 12.
- 12. A method of differentiating between the subtypes of AML cells or the subtypes of AML cells and normal cells in a patient sample comprising the steps of
- a) determining the expression profile of a group of markers in the patient sample and
  - b) concluding from the expression profile which subtypes of AML cells the patient

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sample contains or whether it contains normal cells
characterized in
that the group of markers consists of markers selected independently from the
markers listed in one or more of the tables 1, 2, 13, 14, 17, 25, 27, 35 and 36and
whereby the number of markers in the group is between one and the total number
of markers listed in one or more of the tables 1, 2, 13, 14, 17, 25, 27, 35 and 36.

- 13. The method according to claim 12 characterized in that
- the number of markers in the group is between two and the total number of markers listed in the tables 1, 2, 13, 14, 17, 25, 27, 35 and 36.
  - 14. The method according to claim 12 or 13 characterized in
- that the group of markers consists of all markers listed in one or more of the tables 1, 2, 13, 14, 17, 25, 27, 35 and 36.
  - 15. The method according to any of claims 12 to 14 characterized in
- that three, four or more subtypes of AML cells are determined.
- 16. A method of assessing the efficacy of a test compound for inhibiting leukemia, the method comprising comparing the expression profile of a group of markers in a first sample obtained from the patient and maintained in the presence of the test compound and the expression profile of a group of markers in a second sample obtained from the patient and maintained in the absence of the test compound, wherein a significantly altered expression profile of the group of markers in the first sample, relative to the second sample, is an indication that the test compound is efficacious for inhibiting leukemia in the patient
- 30 characterized inthat the group of markers consists of markers selected independently from the

markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between one and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.

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- 17. A method of assessing the efficacy of a therapy for inhibiting leukemia in a patient, the method comprising comparing the expression profile of a group of markers in a first sample obtained from the patient prior to providing at least a portion of the therapy to the patient and the expression profile of a group of markers in a second sample obtained from the patient following provision of the portion of the therapy, wherein a significantly altered expression profile of the marker(s) in the second sample, relative to the first sample, is an indication that the therapy is efficacious for inhibiting leukemia in the patient characterized in
- that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between one and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.

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- 18. A method of selecting a composition for inhibiting leukemia in a patient, the method comprising:
  - a) separately maintaining aliquots of cells of a patient sample in the presence of a plurality of test compositions;
- 25 c) comparing the expression profile of a group of markers in each of the aliquots, and
  - d) selecting one of the test compositions which induces an altered expression profile of the group of markers in the aliquot containing that test composition, relative to other test compositions
- 30 characterized in that the group of markers consists of markers selected independently from the

markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between one and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.

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- 19. A method of determining new subtypes of leukemia cells, the method comprising:
  - a) determining the expression profile of a group of markers of leukemia cells of unknown subtype
- b) comparing the expression profile of said leukemia cells of ??? subtype to the
   expression profile of a group of markers of leukemia cells of known subtype(s),
   thereby concluding that a new subtype is determined when the expression profile is different to all known subtypes,

characterized in

- that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between one and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.
- 20 20. A method for guiding the therapy of leukemia in a patient depending on the leukemia subtype and/or the risk of relapse of disease, the method comprising:a) determining the expression profile of a group of markers in the patient sample, and
  - b) deciding about the therapy strategy depending on the leukemia subtype and/or the risk of relapse of disease

characterized in

that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between one and the total number of markers listed in the tables 1 to 20, tables 25

or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.

- 21. A method for monitoring the progression of leukemia in a patient, the method comprising:
- a) determining the expression profile of a group of markers in a patient sample at a first point in time, and
  - b) repeating step a) at a subsequent point in time; and
  - c) comparing the expression profile detected in steps a) and b) , and therefrom monitoring the progression of leukemia in the patient,
- that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between one and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.
  - 22. The method of claim 21, wherein between the first point in time and the subsequent point in time, the patient has undergone chemotherapy.
- 20 23. The method according to any of the claims 1 to 22, wherein a transcribed polynucleotide or portion thereof is the marker or at least one of the markers.
  - 24. The method of claim 23, wherein the transcribed polynucleotide is a mRNA.
- 25 25. The method of claim 23, wherein the transcribed polynucleotide is a cDNA.
  - 26. The method according to any of claims 23 to 25, wherein the step of determining the expression profile further comprises amplifying the transcribed polynucleotide.
- 30 27. The method according to any of the claims 23 to 26, wherein the expression profile of the group of transcribed polynucleotides is determined by annealing the

transcribed polynucleotides with a complementary polynucleotide or a portion thereof under stringent hybridization conditions.

- 28. The method according to any of the claims 1 to 27, wherein the patient sample is blood or bone marrow.
  - 29. The method according to any of the claims 1 to 22, wherein a protein is the marker or at least one of the markers.
- 10 30. The method of claim 29, wherein the expression profile of the proteins is detected using a reagent which specifically binds to one of the proteins.
  - 31. The method of claim 30, wherein the reagent is selected from the group consisting of an antibody, an antibody derivative, and an antibody fragment.
- 32. The method according to any of claims 16 to 31
  characterized in that
  the number of markers in the group is between two and the total number of
  markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36,
  38, 39, 41, 42.
- 33. The method according to any of claims 16 to 32
  characterized in
  that the group of markers consists of all markers listed in one or more of the tables
  1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.
  - 34. A kit for assessing the suitability of each of a plurality of compounds for inhibiting leukemia in a patient, the kit comprising:
- a) (optionally) a plurality of compounds; and
  - b) a reagent for assessing the expression profile of a group of markers

characterized in

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that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between one and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.

- 35. A kit for assessing whether a patient is afflicted with leukemia, the kit comprising reagents for assessing the expression profile of a group of markers
- that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between one and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.
  - 36. A kit for assessing the presence of human leukemia cells, the kit comprising an antibody, wherein the antibody specifically binds with a protein corresponding to a marker
- characterized in
   that the marker is selected from the tables 1 to 20, tables 25 or 27 or tables 29, 30,
   32, 33, 35, 36, 38, 39, 41, 42.
- 37. A kit for assessing the leukemia cell carcinogenic potential of a test compound, the kit comprising leukemia cells and a reagent for assessing expression of a marker, wherein the marker is selected from the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.
- 38. A protein or mRNA, cDNA or cRNA corresponding to a marker selected from the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 for the treatment of leukemia.

39. A method for the preparation of a pharmaceutical composition for the treatment of leukemia

characterized in

- that a protein corresponding to a marker selected from the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 is admixed with pharmaceutical compounds.
- 40. A method for the preparation of a pharmaceutical composition for the treatment of leukemia

characterized in

that a vector comprising a polynucleotide encoding a protein corresponding to a marker selected from the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 is admixed with pharmaceutical compounds.

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41. A method for the preparation of a pharmaceutical composition for the treatment of leukemia

characterized in

that an antisense oligonucleotide complementary to a polynucleotide encoding a protein corresponding to a marker selected from the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 is admixed with pharmaceutical compounds.

- 42. Use of a marker or a group of markers selected individually from one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 for the determination of leukemia cells, the type or subtype of leukemia cells.
- 43. Use of a marker or a group of markers selected individually from one or more of the tables 1, 2, 13, 14, 17, 25, 27, 35 or 36 for the determination of the subtype of AML cells.

44. A composition comprising a group of markers and substances chemically different to the markers

characterized in

that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42 and whereby the number of markers in the group is between one and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.

10 45. The composition according to claim 44

characterized in

that the group of markers consists of all markers listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38, 39, 41, 42.

15 46. The composition according to claim 45

characterized in

that the group of markers consists of all markers listed in one or more of the tables 14 or tables 16 to 20 or table 29 or 30.

20 47. The composition according to claim 46

characterized in

that the group of markers consists of all markers listed in the tables 16 to 20 or table 29 or 30.

25 48. The composition according to claim 44 to 47

characterized in

that the markers are polynucleotides or oligonucleotides and are bound to a solid phase in the form of an array.

30 49. A method of determining the subtypes of ALL cells in a patient sample comprising the steps of

- a) determining the level of expression of a group of markers in the patient sample and
- b) concluding from the differences in the level of expression which subtypes of ALL cells the patient sample contains
- 5 characterized in

that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 18, 32 or 33 and whereby the number of markers in the group is between two and the total number of markers listed in the tables 18, 32 or 33.

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50. The method according to claim 49

characterized in

that the group of markers consists of all markers listed in one or more of the tables 18, 32 or 33.

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- 51. A method of determining the subtypes of CLL cells in a patient sample comprising the steps of
  - a) determining the level of expression of a group of markers in the patient sample and
- b) concluding from the differences in the level of expression which subtypes of CLLcells the patient sample contains

characterized in

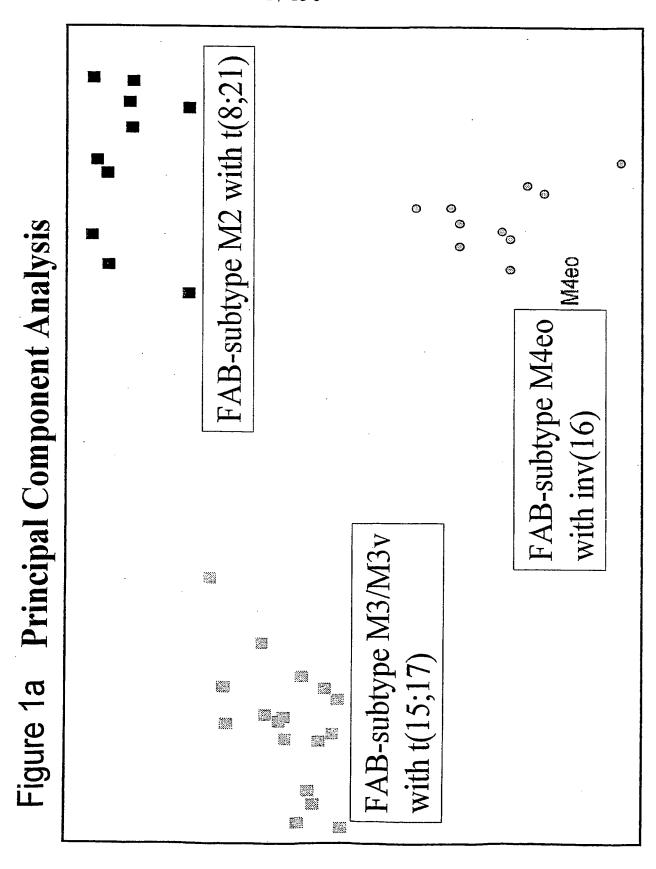
that the group of markers consists of markers selected independently from the markers listed in one or more of the tables 38 or 39 and whereby the number of markers in the group is between two and the total number of markers listed in the tables 38 or 39.

52. The method according to claim 51 characterized in

that the group of markers consists of all markers listed in one or more of the tables

38 or 39.

- 53. A method of determining whether a patient sample contains leukemia cells or other cells and at the same time determining the type and subtype of leukemia cells,
- 5 comprising
  - a) providing a patient sample,
  - b) isolating RNA from the patient sample, transcribing the RNA into cDNA and transcribing the cDNA into cRNA while simultaneously labelling the cRNA
- c) hybridising the cRNA to a microarray having attached thereto a group of markers selected from the group listed in one or more of the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38,. 39, 41, 42 and whereby the number of markers in the group is between two and the total number of markers listed in the tables 1 to 20, tables 25 or 27 or tables 29, 30, 32, 33, 35, 36, 38,. 39, 41, 42, and d) determining the level of expression of a marker or a group of markers.
- 15
- 54. Use of a marker or a group of markers selected from the group of members contained in the appended tables for determining whether a patient sample contains leukemia cells or other cells.
- 20 55. Use of claim 54 wherein said determination comprises the simultaneous determination of the type and subtype of leukemia cells.



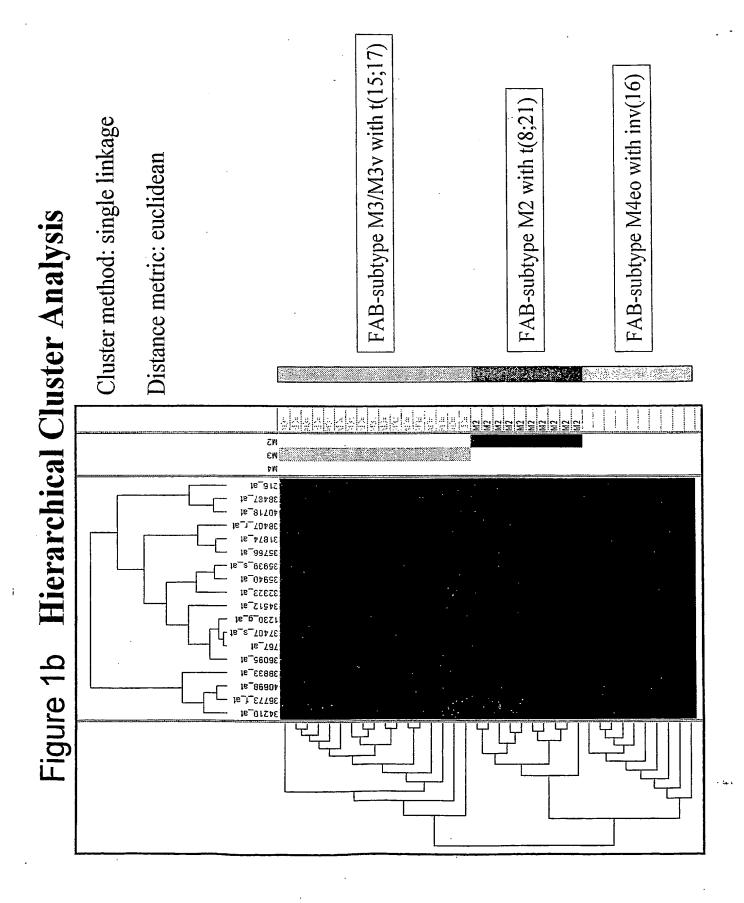
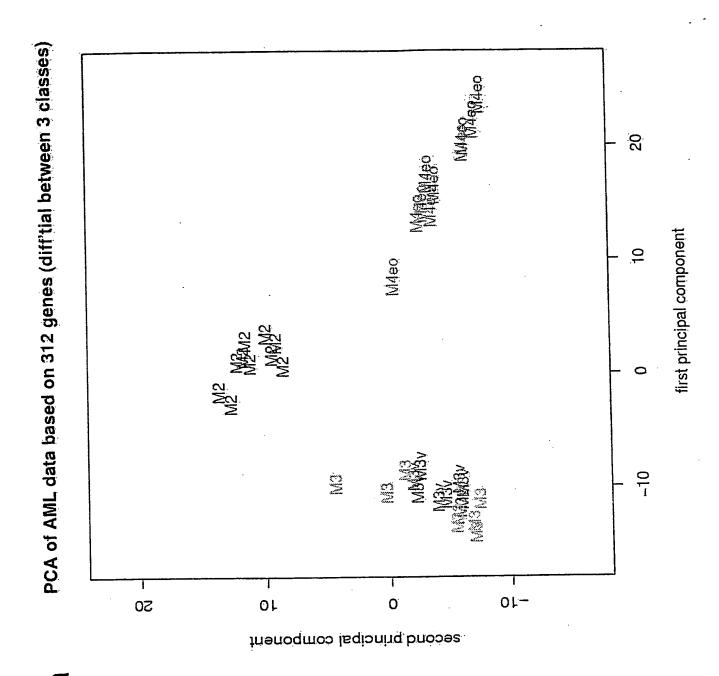
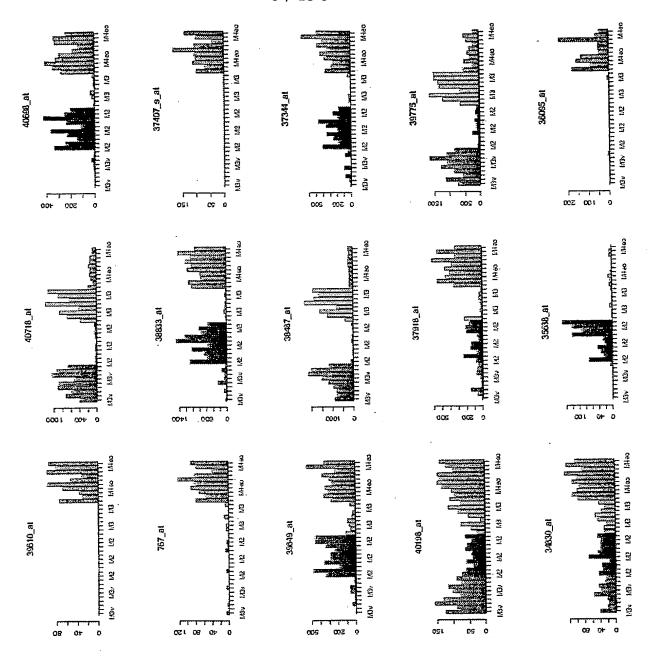


Figure 2 Classification Accuracy

accuracy	ассигасу - ((15;17) - 1(8;21)	.21) ((15,17) - inv(16) inv(16) - t(8,21)	inv(16) - t(8;21)	1(8;21) - R t	1(8,21) - R 1(15,17) - R inv(16) - R
Control of the Contro					
U78556		-			1.00
M98539					1.00
Y07846		·		1,00	
M63582				1.00	
99806N		1.00			
J03853			1.00	1.00	
M26326	1.00			1.00	
120433			1.00	1,00	
X64624	1.00		1.00	1.00	
N99340			1.00		1,00
M81141	1.00				1:00
AF013570			1.00		1.00
A1207842		1.00			1.00 1.00
D87433	1.00	 -		1.00	
X00457	1.00	-			
X96719		1.00			1,00
AF013611	1.00			1.00	
AF001548			1.00		1,00



Fig



igure 3b

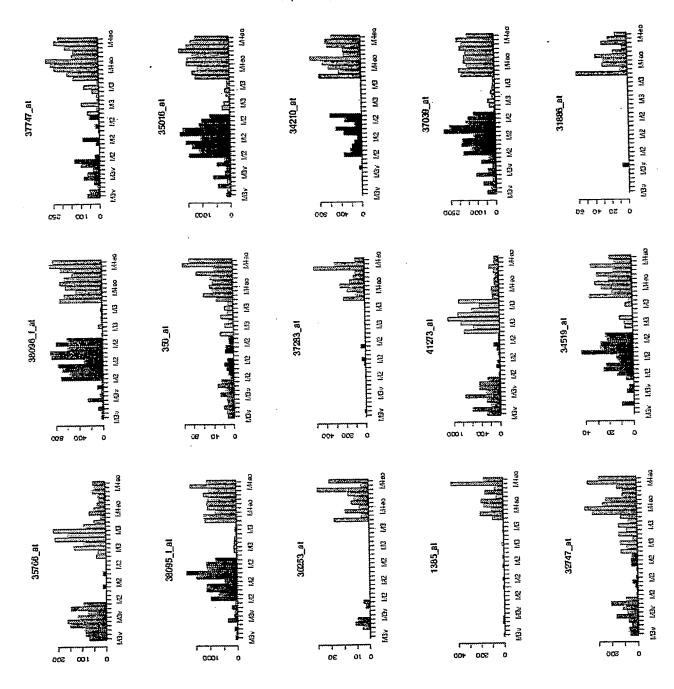
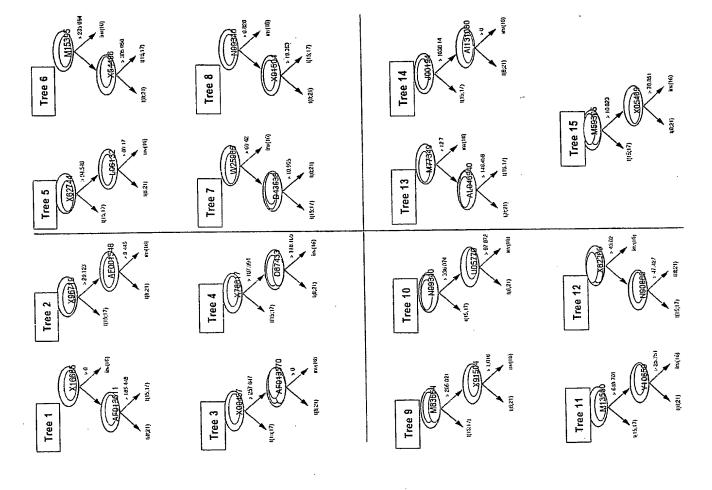


Figure 3b2



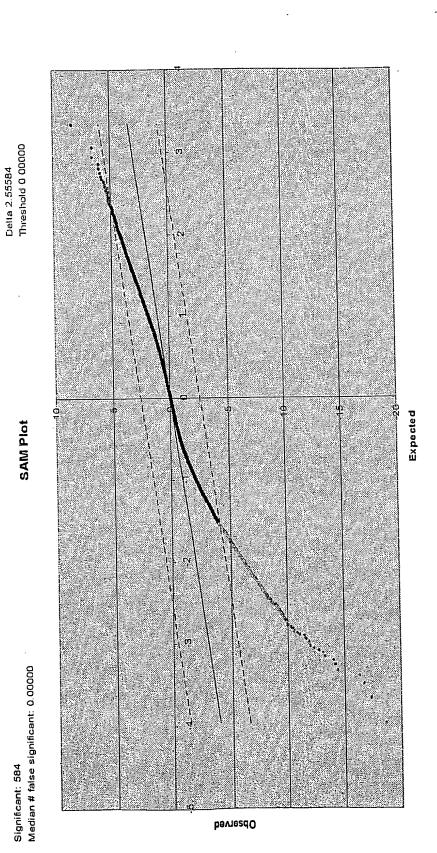
<u>با</u>

Decision trees according to IE

# 5a) Pairwise Comparison of Normal BM and AMI

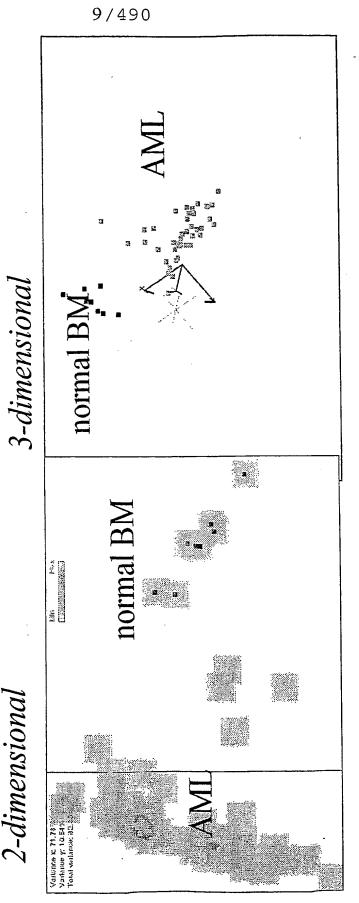
Significance Analysis of Microarrays:

Selection of 127 differentially expressed genes based on a permutation test (K-Nearest Neighbour Imputer)



### 5b) Principal Component Analysis

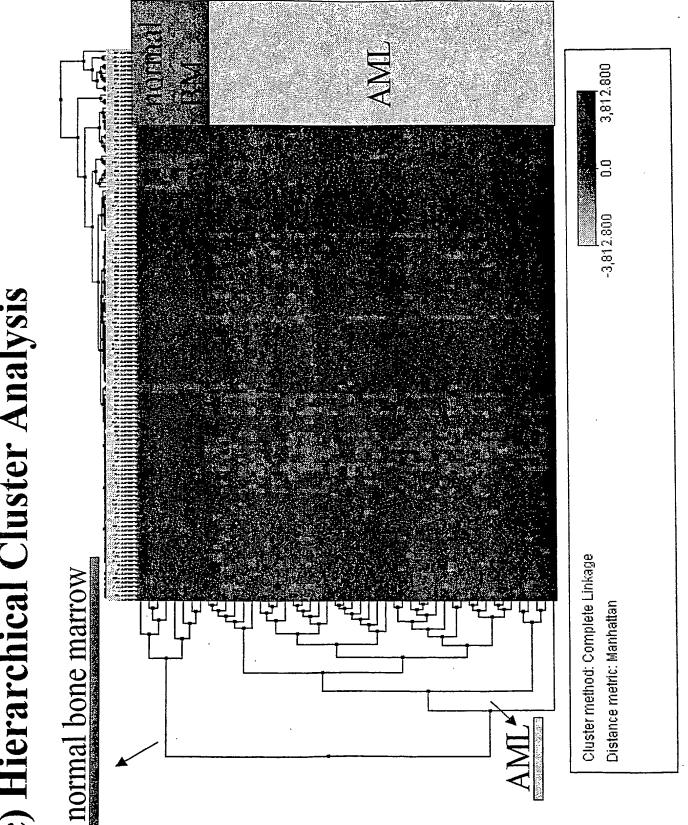
based on 127 significantly differentially expressed genes as selected by  $SAM = \underline{Significance \ Analysis}$  of  $\underline{Microarrays}$ 



|| $\parallel$ normal BM AML

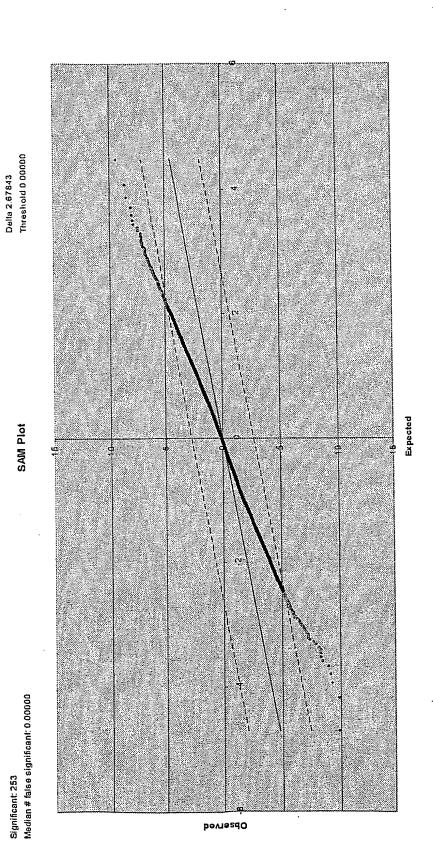
bone marrow from healthy volunteers, n = 8 acute myeloid leukemia, n = 48

### 5c) Hierarchical Cluster Analysis



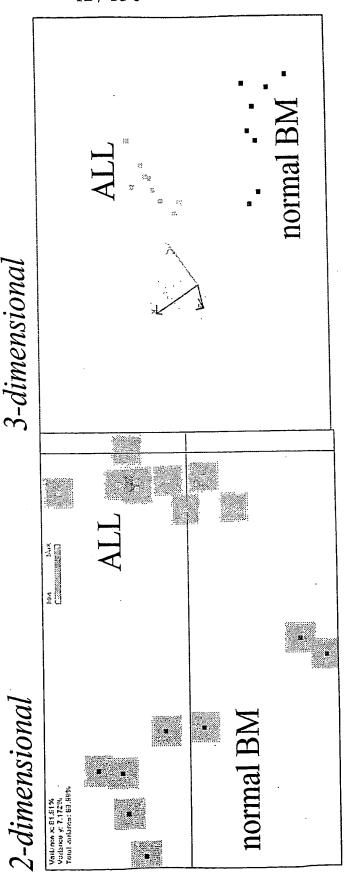
## 6a) Pairwise Comparison of Normal BM and ALL

Selection of 186 differentially expressed genes based on a permutation test (K-Nearest Neighbour Imputer) Significance Analysis of Microarrays:

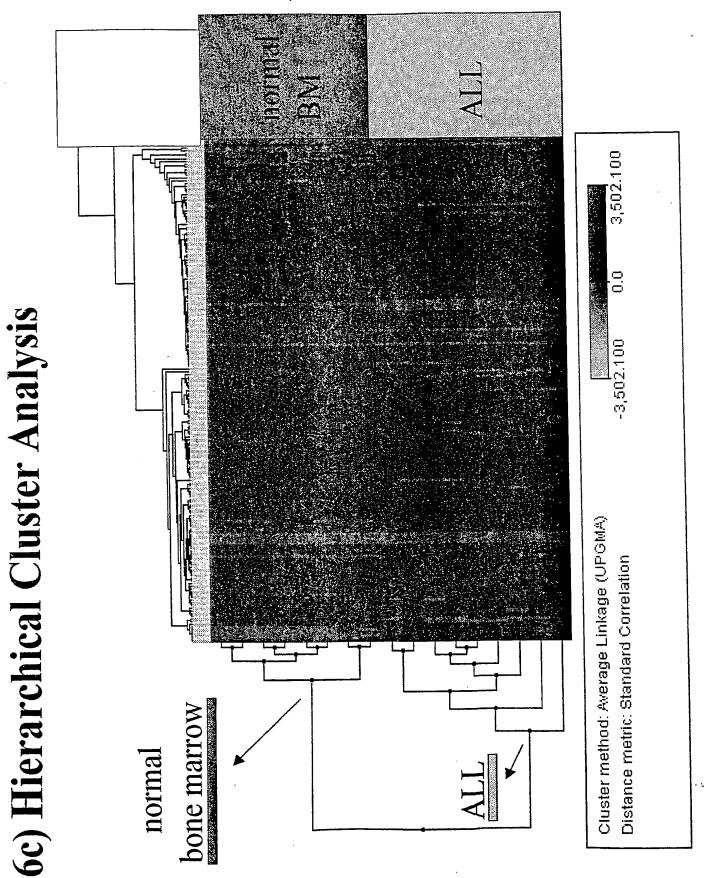


### 6b) Principal Component Analysis

based on 186 significantly differentially expressed genes as selected by SAM = Significance Analysis of Microarrays

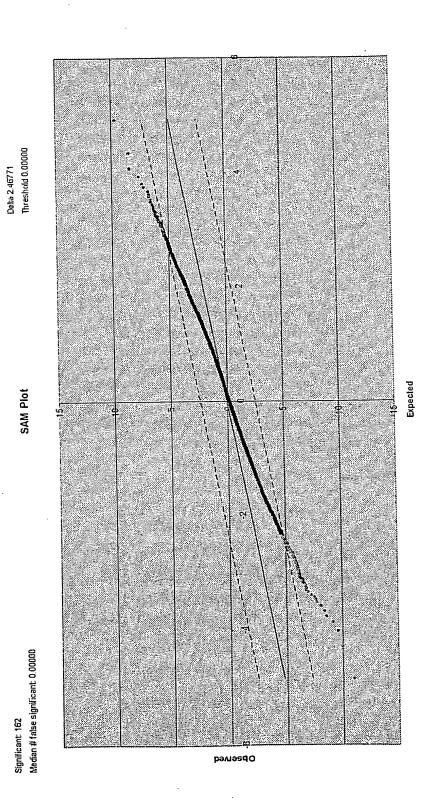


bone marrow from healthy volunteers, n =8 akute lymphoblastic leukemia, n = 9 11  $\|$ normal BM



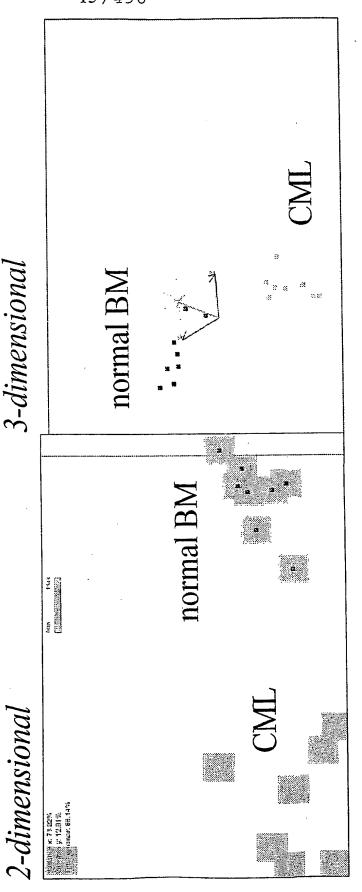
# 7a) Pairwise Comparison of Normal BM and CMI

Selection of 162 differentially expressed genes based on a permutation test (K-Nearest Neighbour Imputer) Significance Analysis of Microarrays:



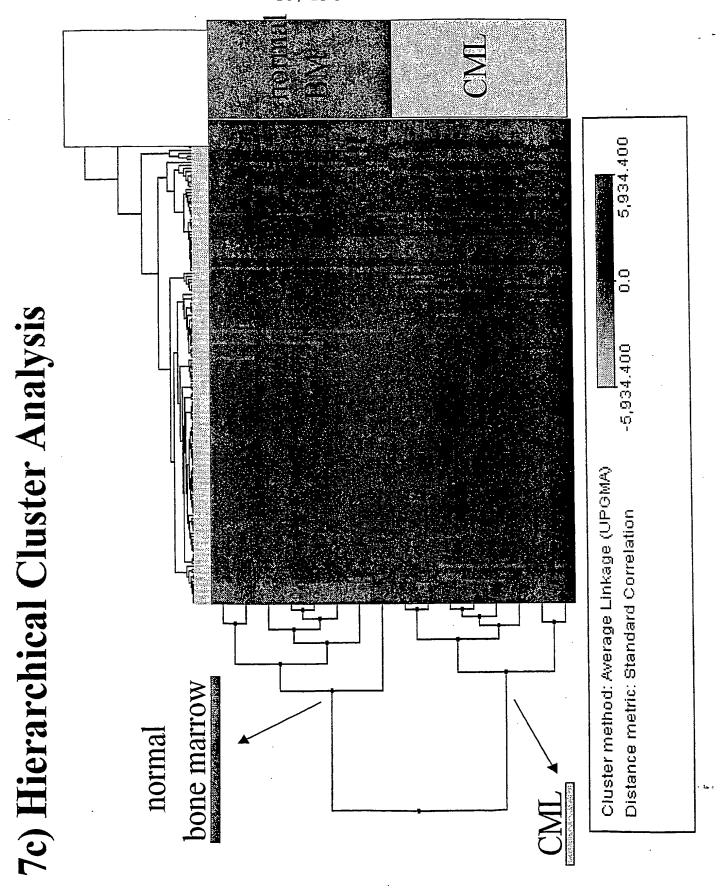
## 7b) Principal Component Analysis

based on 200 significantly differentially expressed genes as selected by SAM = Significance Analysis of Microarrays



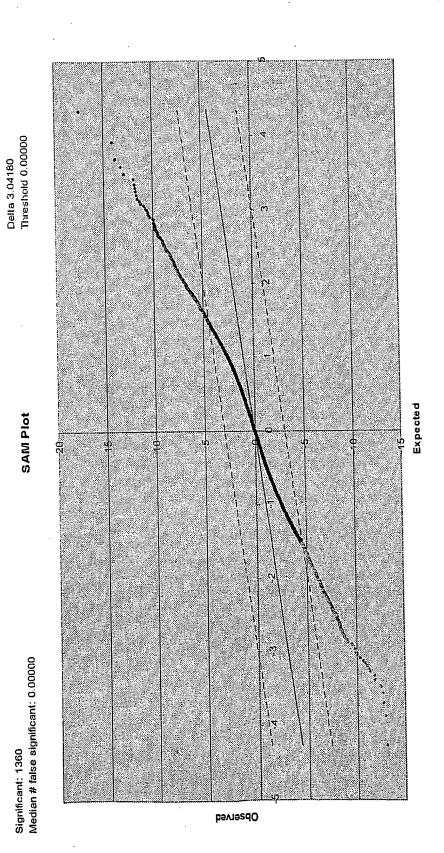
|| normal BM CMI

bone marrow from healthy volunteers, n =8 chronic myeloid leukemia, n = 8



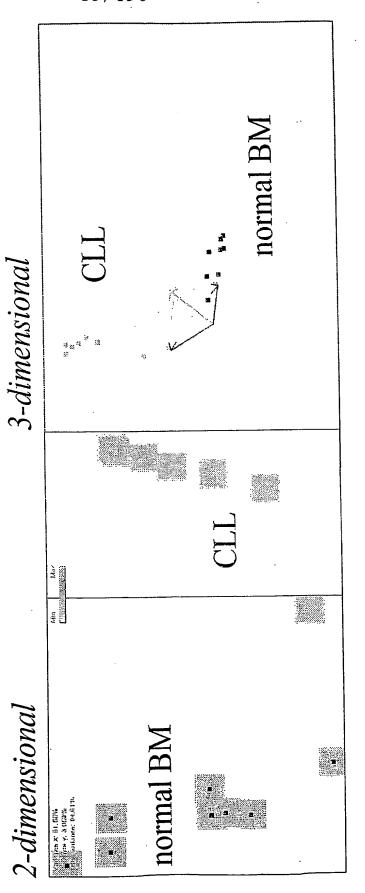
## 8a) Pairwise Comparison of Normal BM and CLI

Selection of 200 differentially expressed genes based on a permutation test (K-Nearest Neighbor Imputer) Significance Analysis of Microarrays

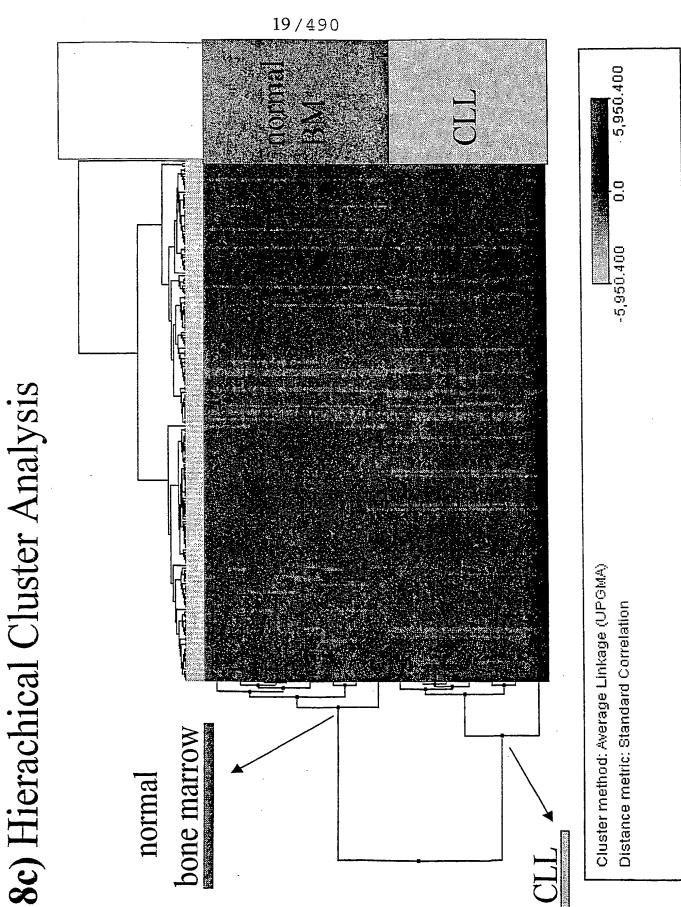


#### 8b) Principal Component Analysis

based on 200 significantly differentially expressed genes as selected by SAM = Significance Analysis of Microarrays

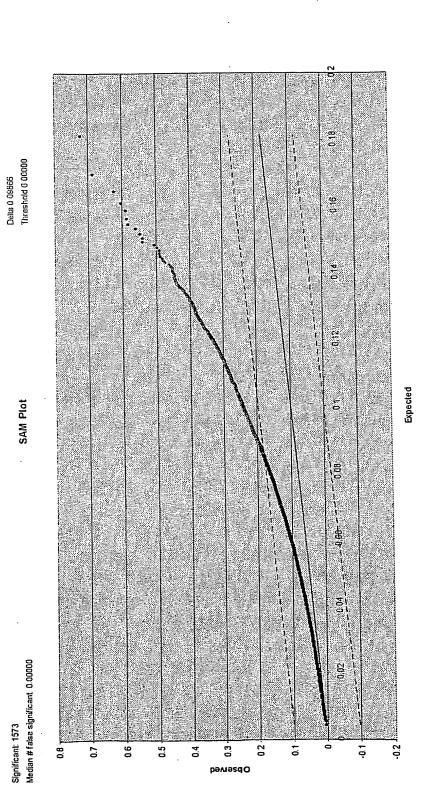


bone marrow from healthy volunteers, n =8 chronic lymphatic leukemia, n = 7normal BM



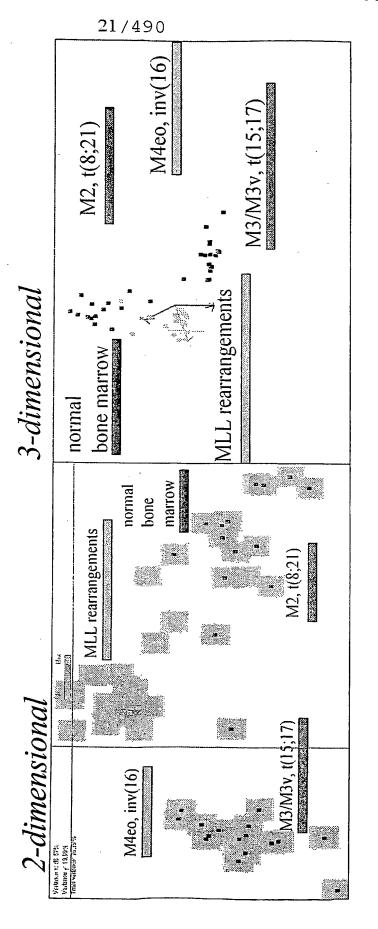
#### 9a) AML-WHO Classification

Selection of 124 differentially expressed genes based on a permutation test (K-Nearest Neighbor Imputer) Significance Analysis of Microarrays:



## 9b) Principal Component Analysis

based on 124 significantly differentially expressed genes as selected by SAM = Significance Analysis of Microarrays

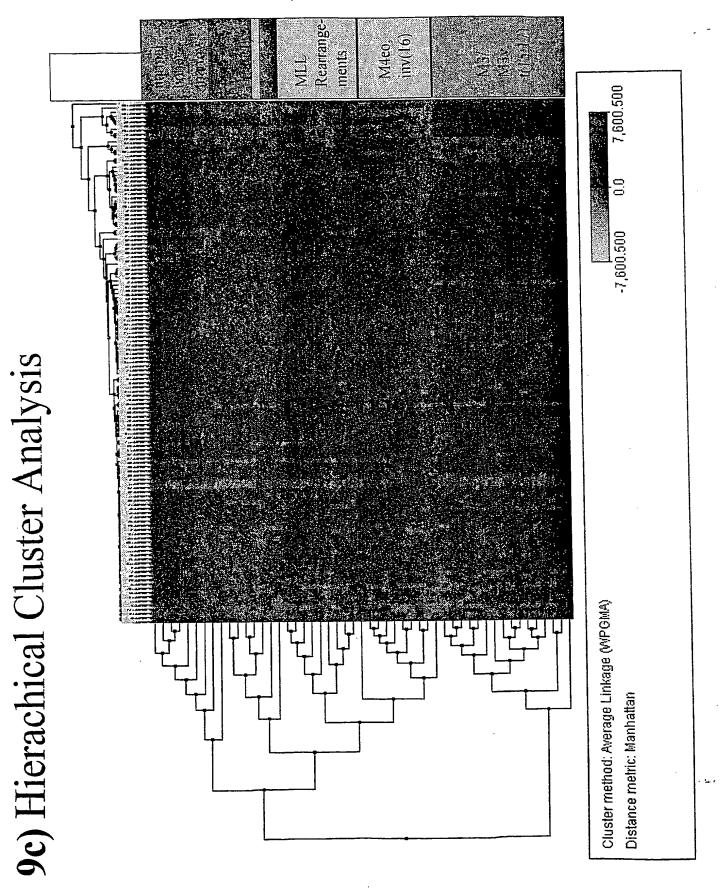


AML = normal BM =

bone marrow from healthy volunteers, n =8 4 distinct cytogenetic subgroups, n = 48

BNSDOCID: <WO\_\_\_\_03039443A2\_I\_>

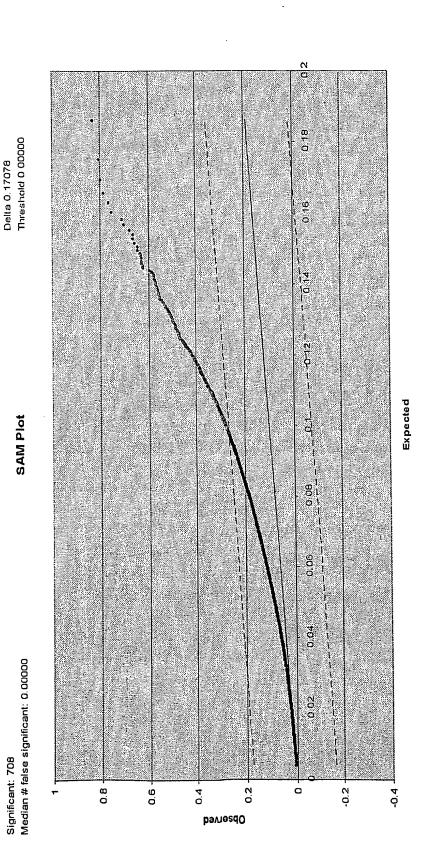
22/490



# 10a) Comparison of Normal BM versus Leukemia

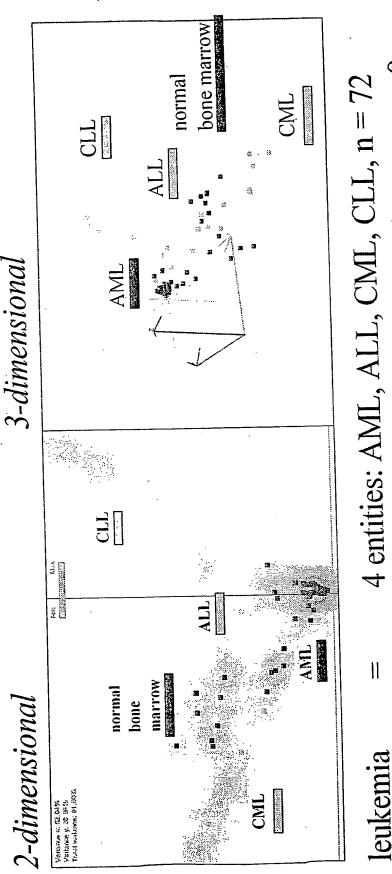
Significance Analysis of Microarrays:

Selection of Top100 differentially expressed genes based on a permutation test (K-Nearest Neighbour Imputer)



## 10b) Principal Component Analysis

based on 100 significantly differentially expressed genes as selected by SAM = Significance Analysis of Microarrays



leukemia = normal BM =

bone marrow from healthy volunteers, n =8

BNSDOCID: <WO 03039443A2\_IL:

25/490

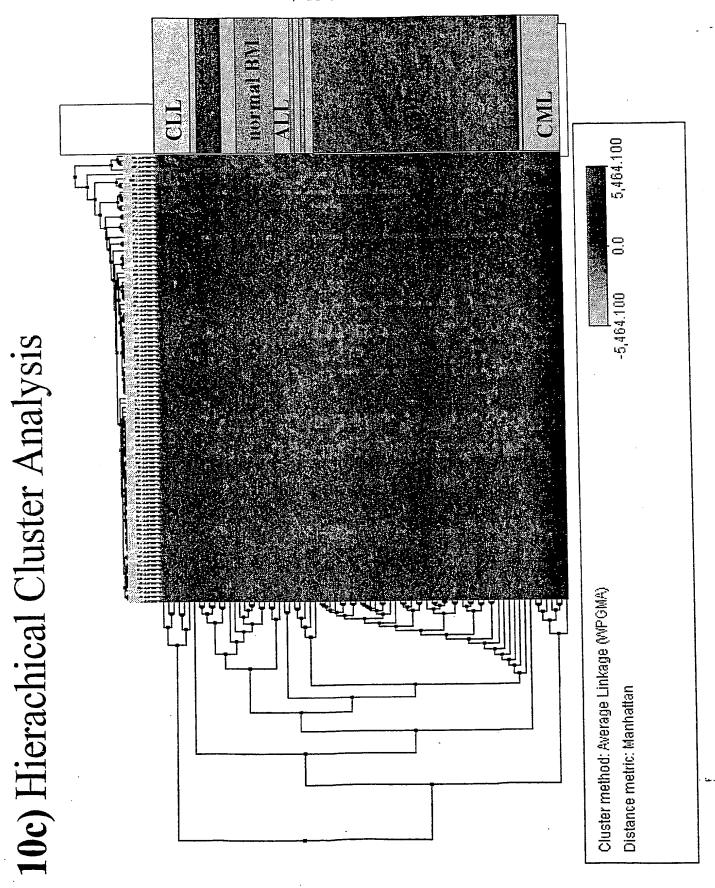
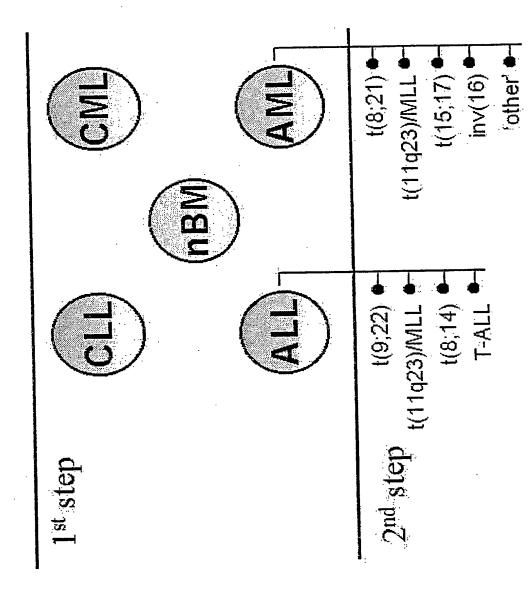
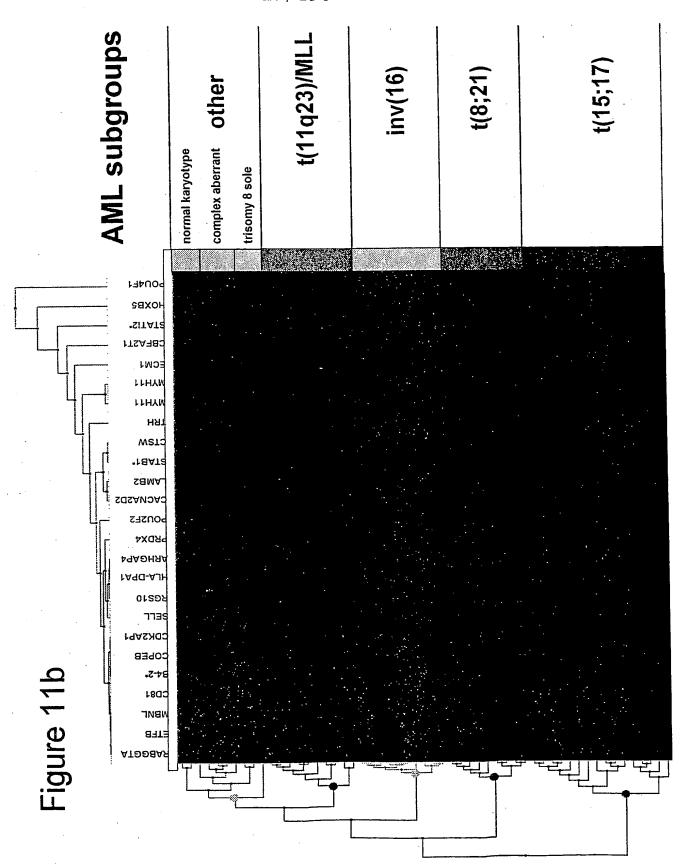


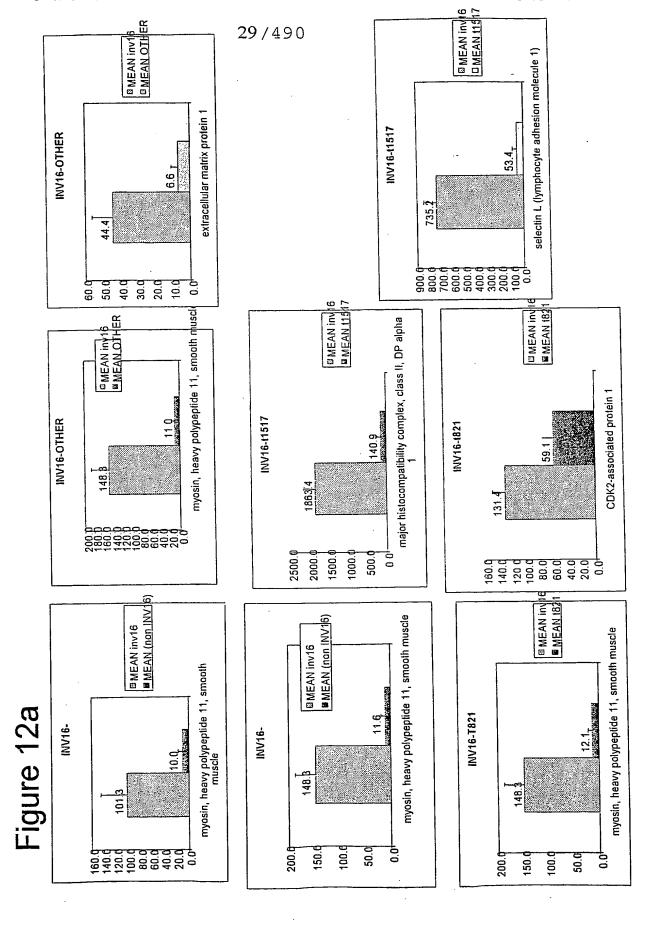
Figure 11a

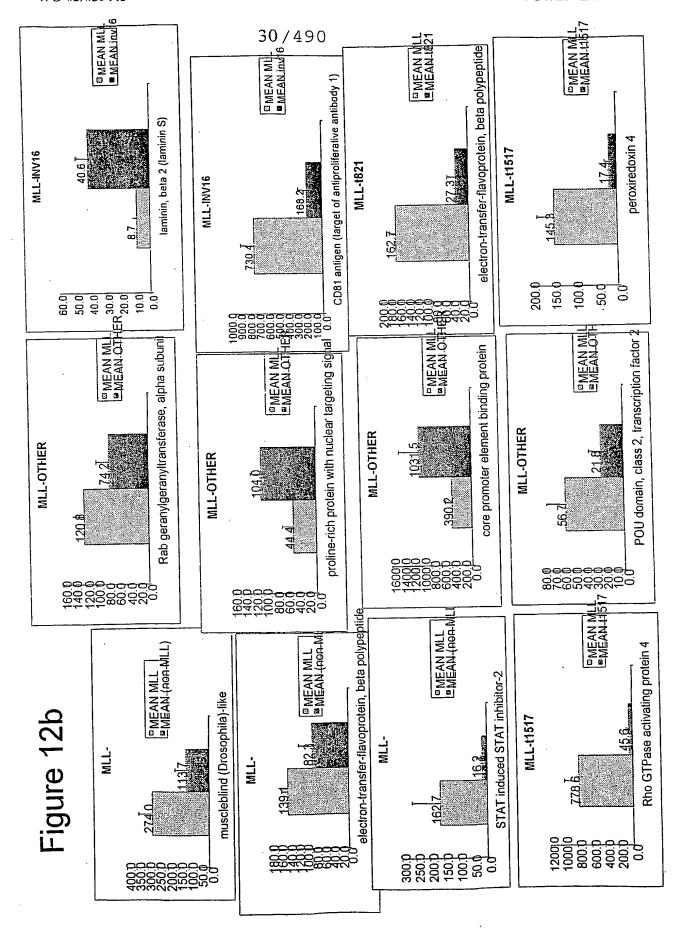


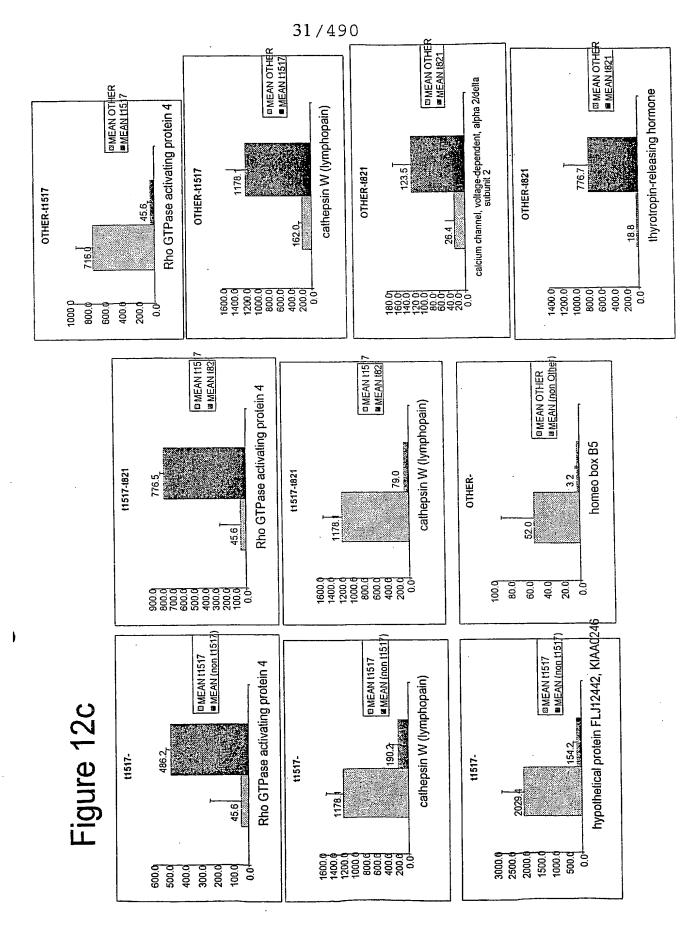
27/490



ALL subgroups ארסרצ OTFG CD3D WWE nuknown\* KIAA0870° "AOGNOM HELO1 AGA WAB WAB **LANNTO** CTNNA1 Figure 11c **SCYA3**  $\Gamma$  $\lambda N$ аят .LIS **SAXNA** 







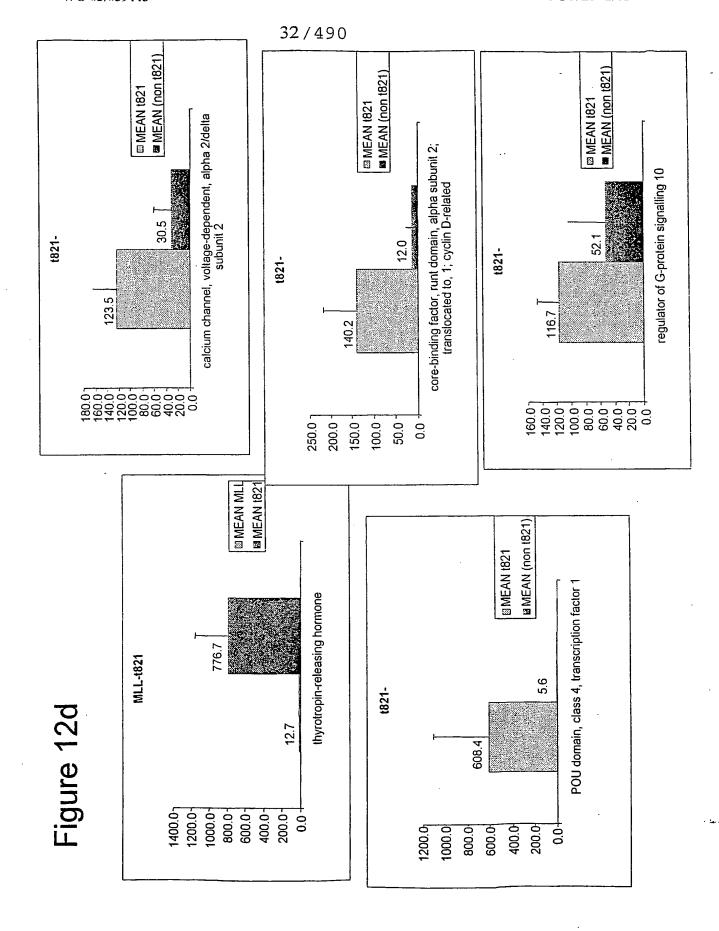
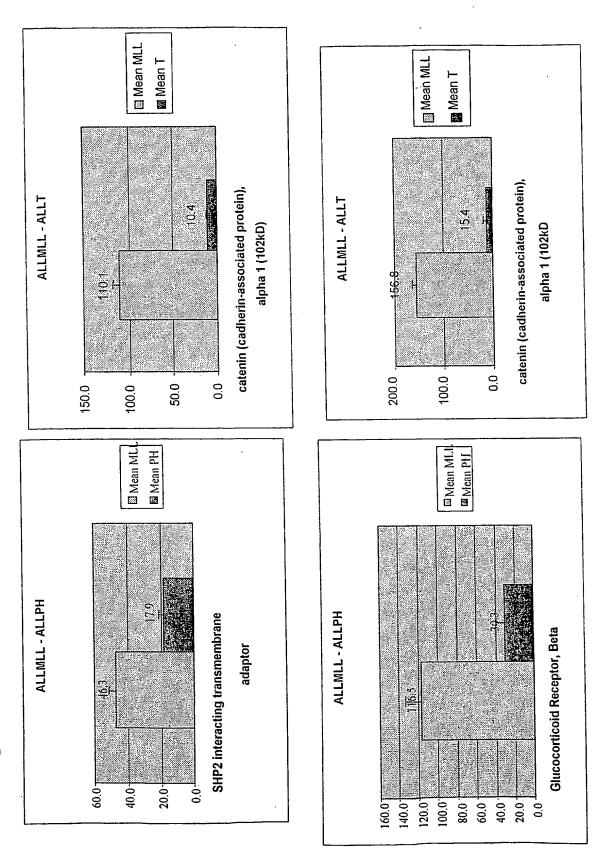
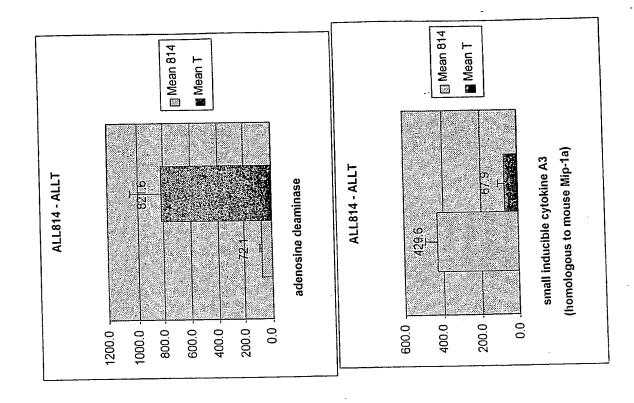
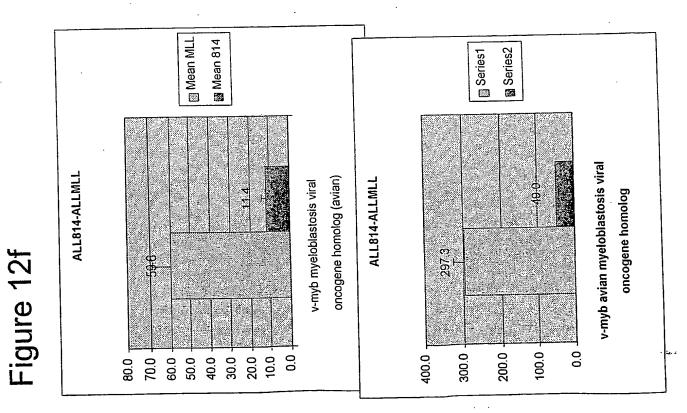


Figure 12e



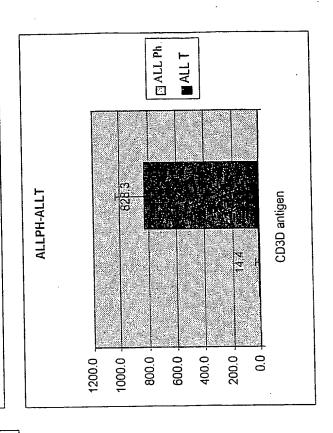
34/490

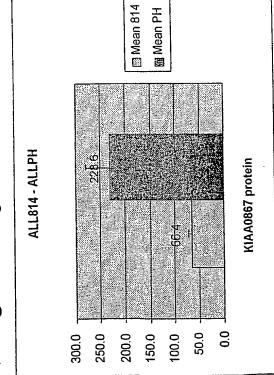


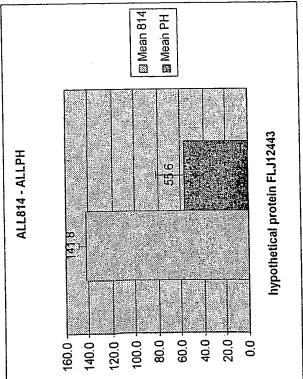


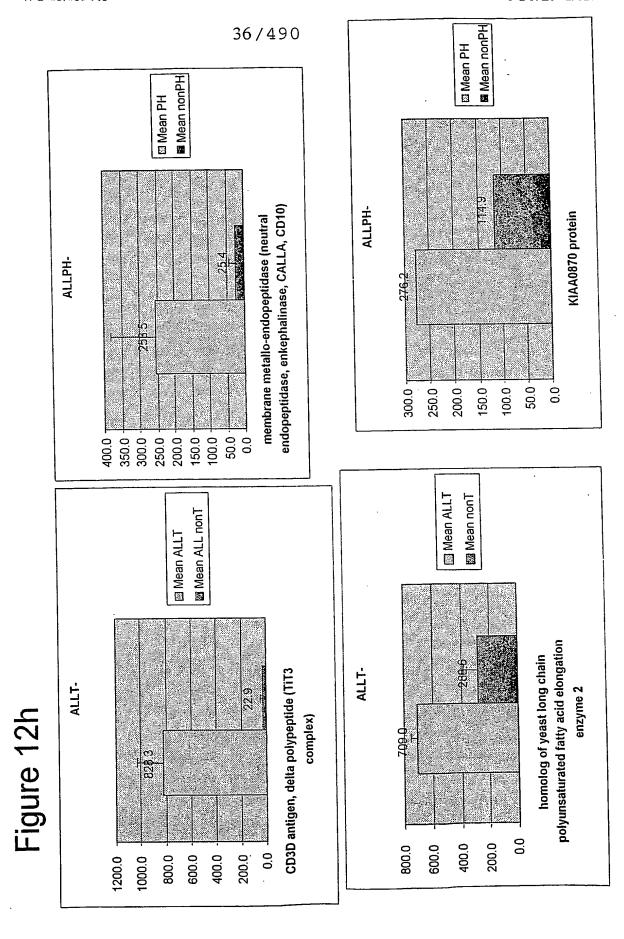
T cell receptor beta locus

🔳 Mean PH Mean T 25176 ALLPH-ALLT 159.7 0.0 3600.0 2400.0 Mean 814 📾 Mean PH Figure 12g

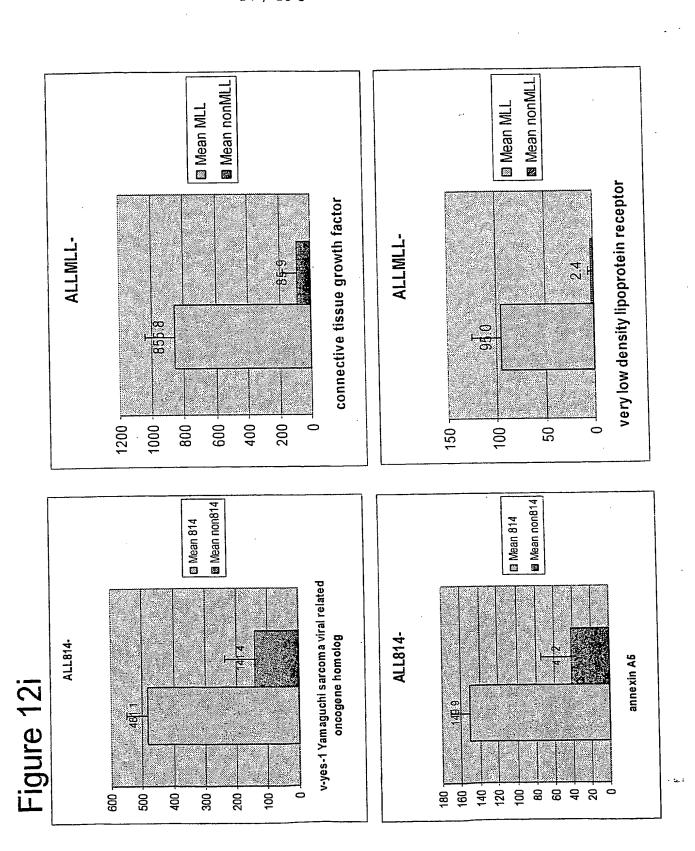








37/490



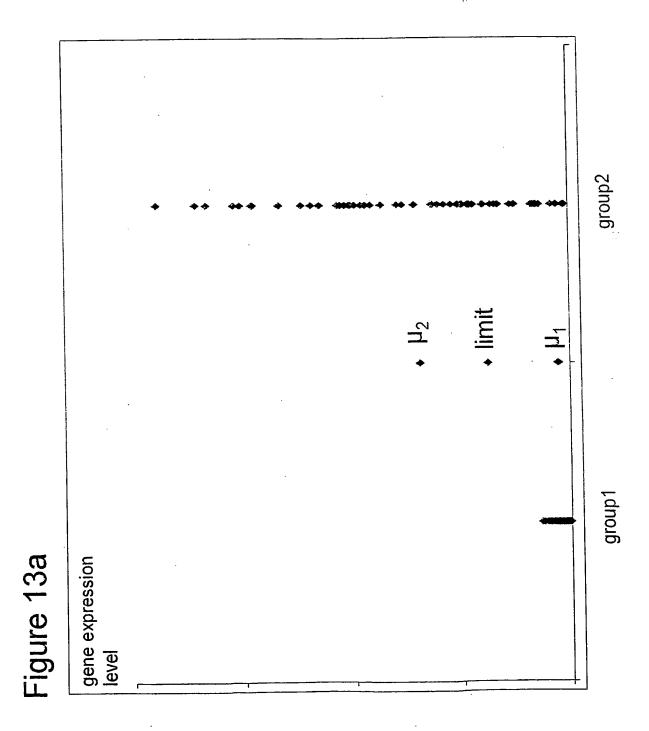
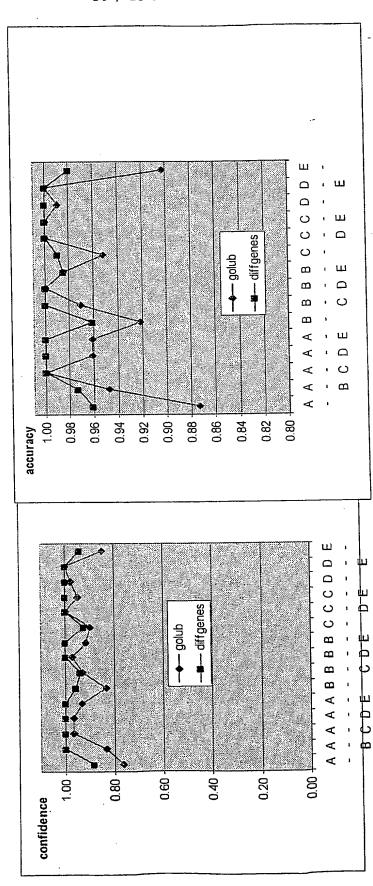
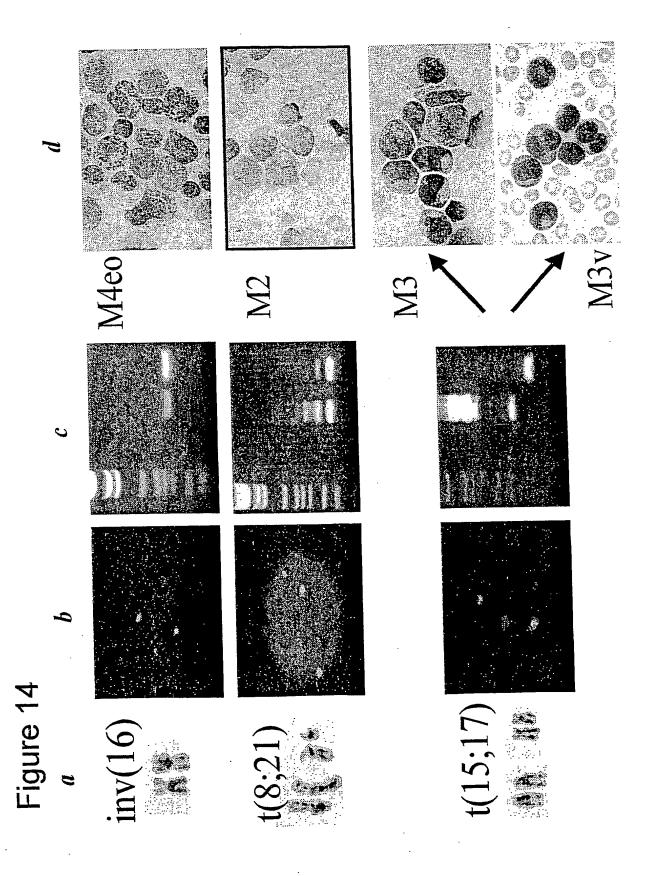
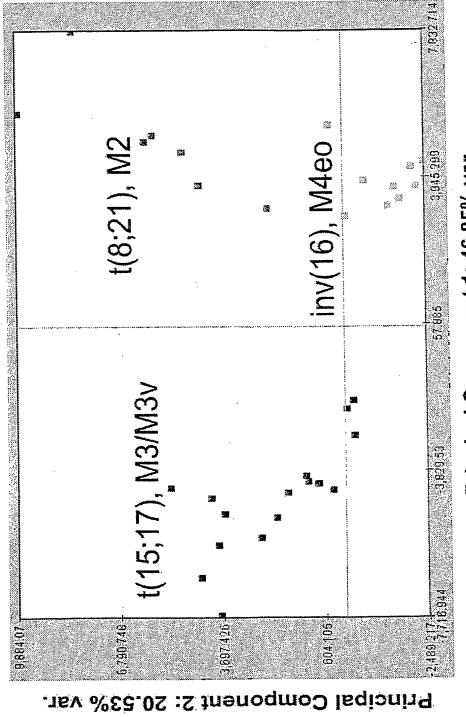


Figure 13b









Principal Component 1: 46.85% var.

(16), AML M4eo

o 📓 t(8;21), AML M2

t(15;17), AML M3/M3v

BNSDOCID: <WO\_\_\_\_03039443A2\_I\_>

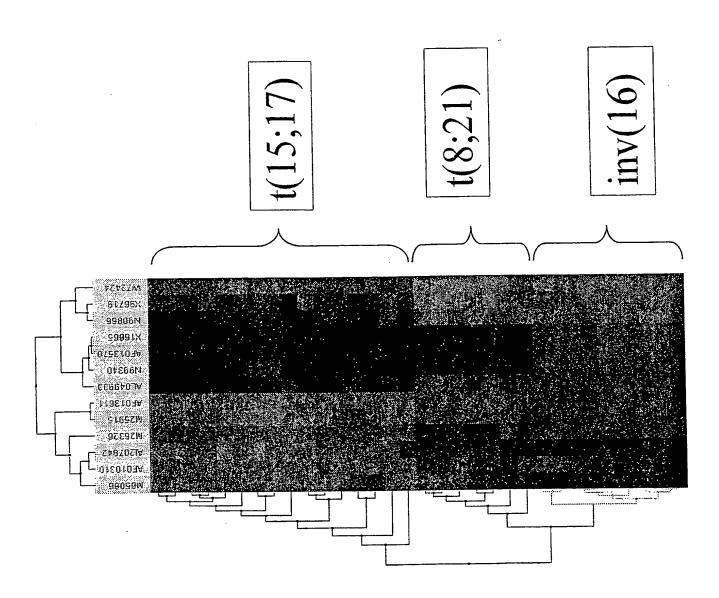


Figure 16

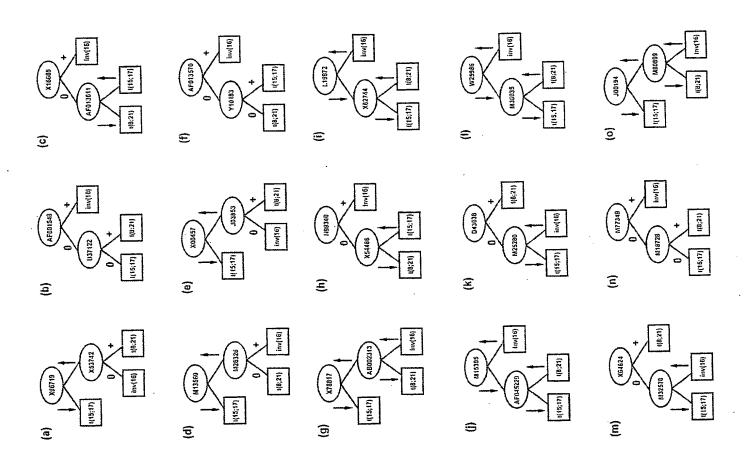
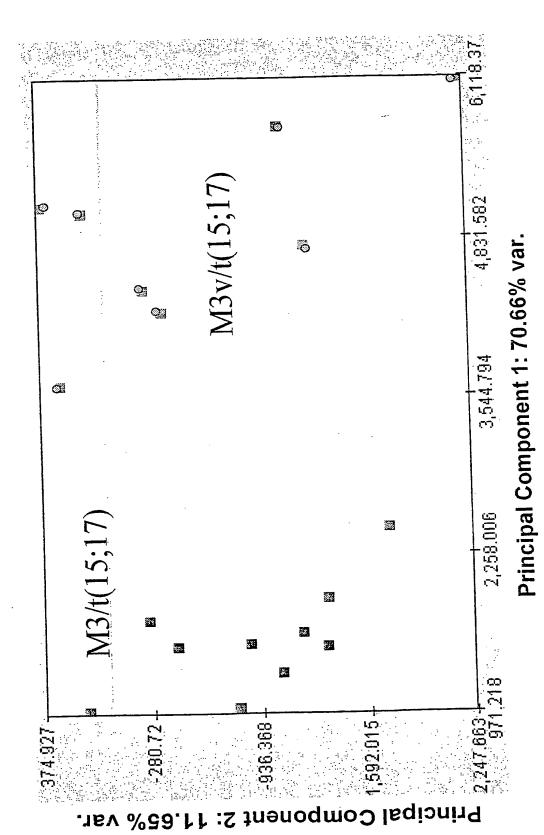
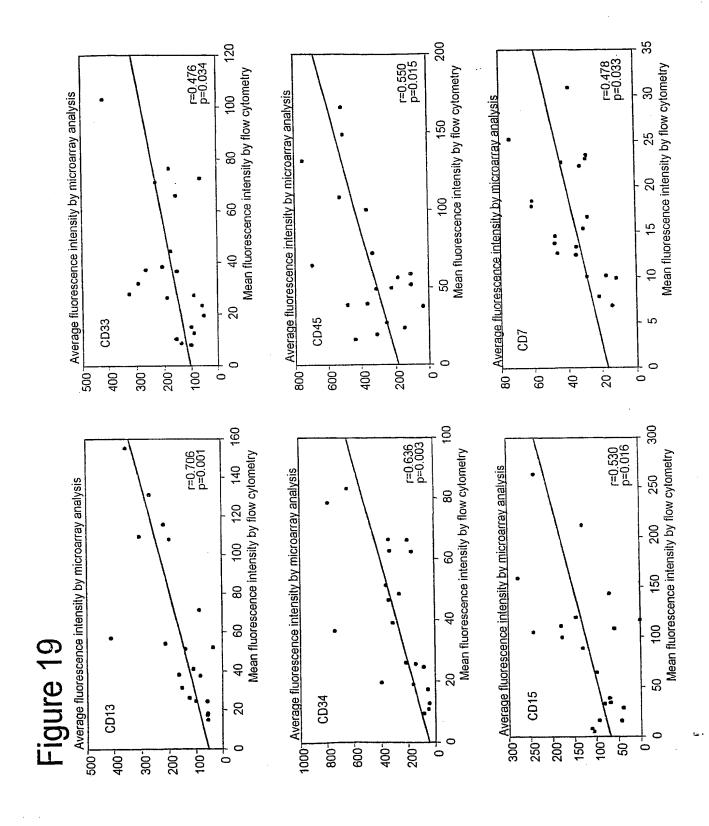
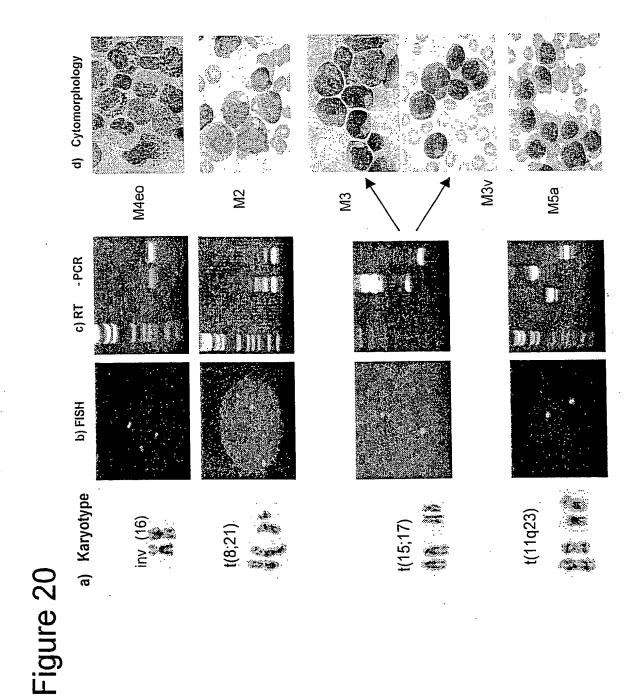


Figure 18







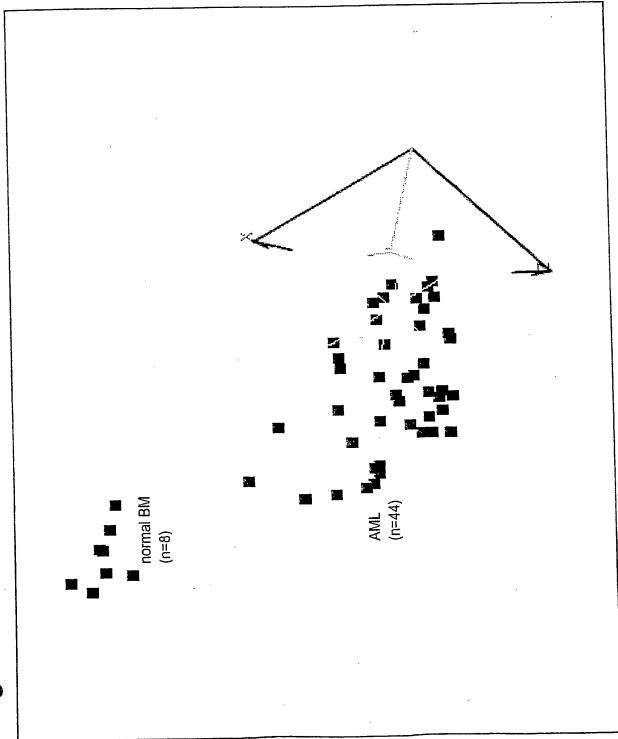
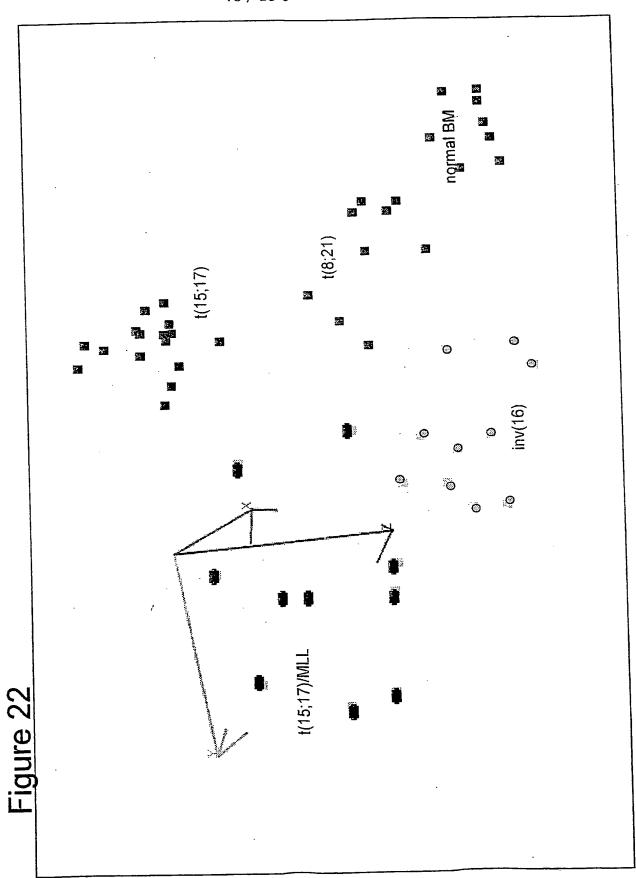
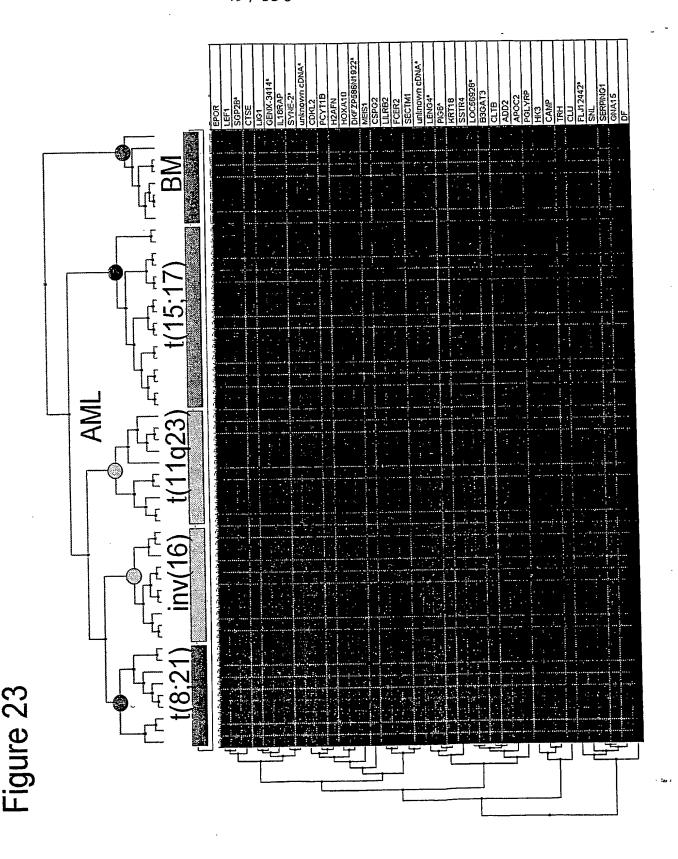


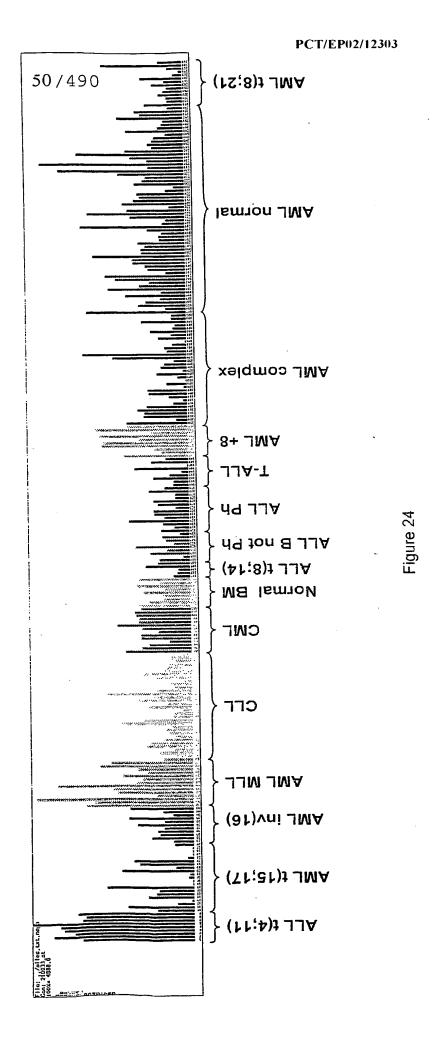
Figure 21



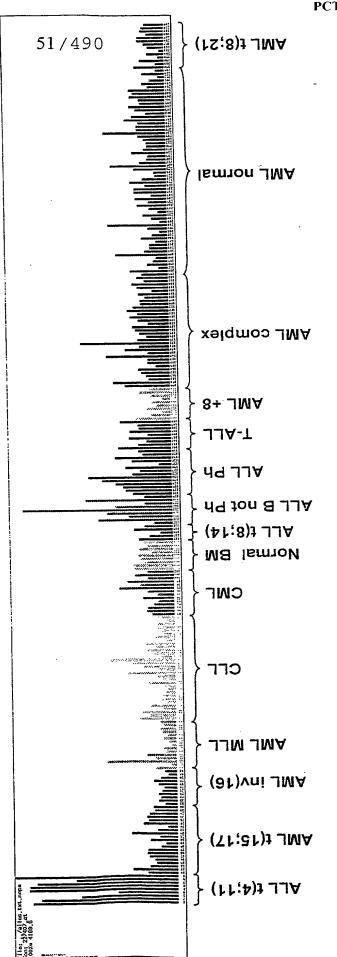
49/490



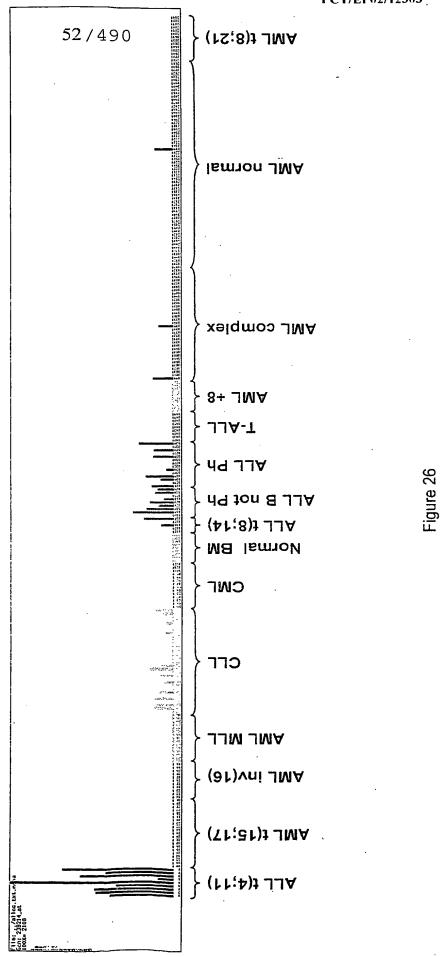
219033\_at, FLJ21308, ALL t(4;11) vs. all other

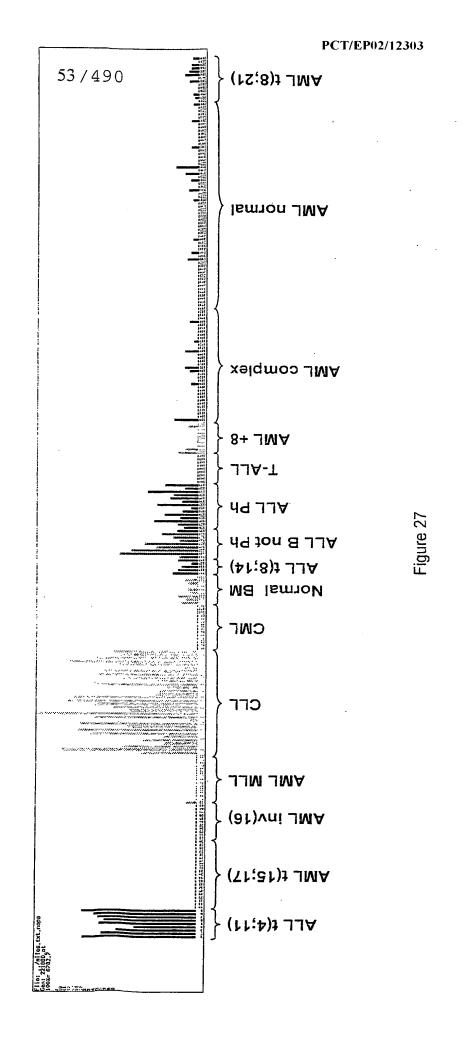


## 227407\_at, ALL t(4;11) vs. all others



## 239214\_at, ALL t(4;11) vs. all others





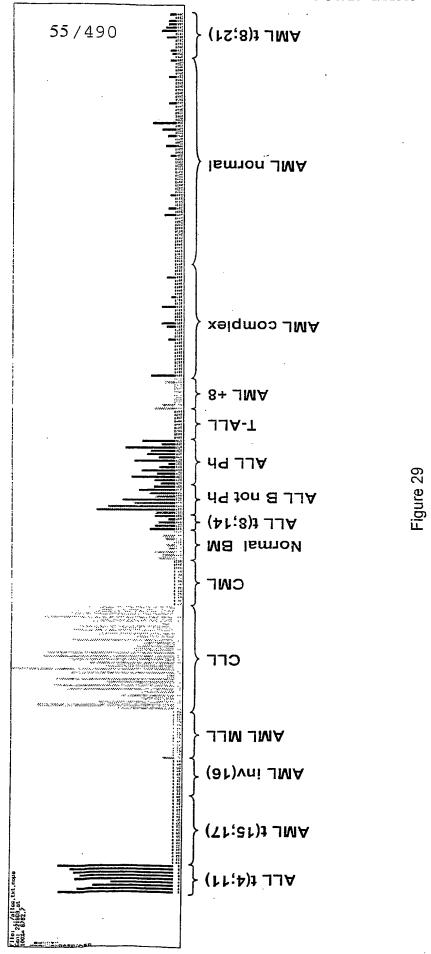
BNSDOCID: <WO\_\_\_\_\_03039443A2\_I\_>

225653\_at, ALL t(4;11) vs. AML inv(16)

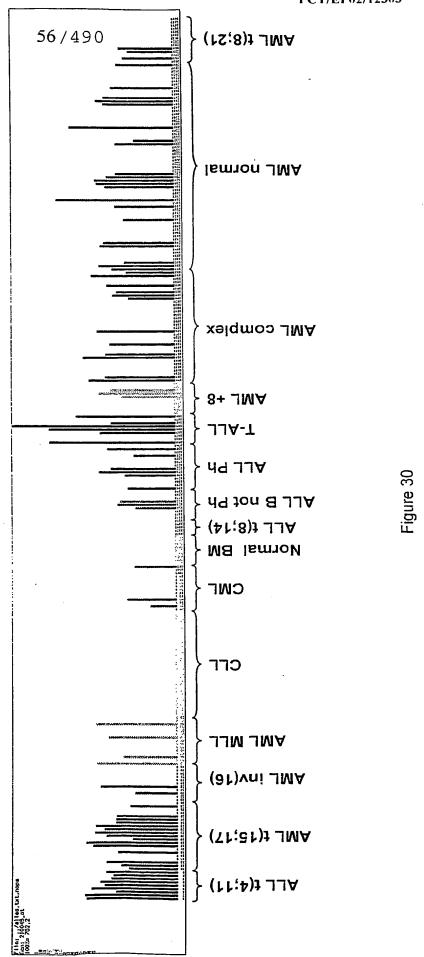
(12;8)1 JMA 54/490 AML normal AML complex 8+ JMA JJA-T ALL Ph ALL B not Ph ALL t(8;14) Normal BM CWL CLL AML MLL (81)vni JMA (Tr;31)1 JMA ALL t(4;11)

PCT/EP02/12303

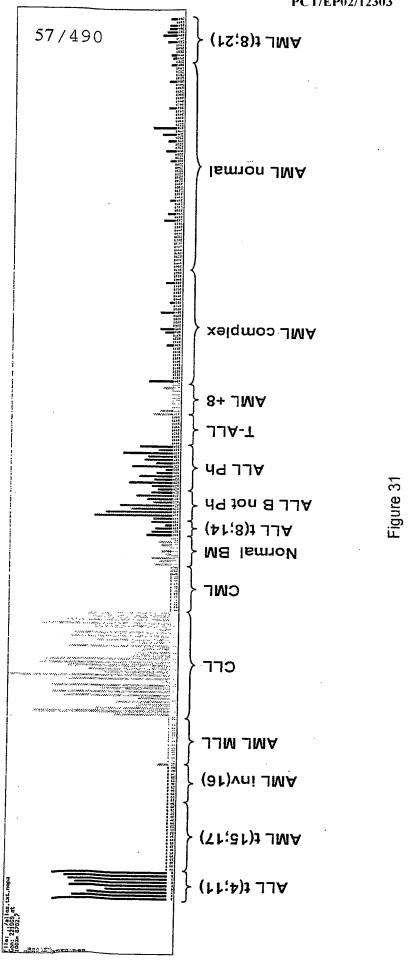
## 221969\_at, ALL t(4;11) vs. AML MLL



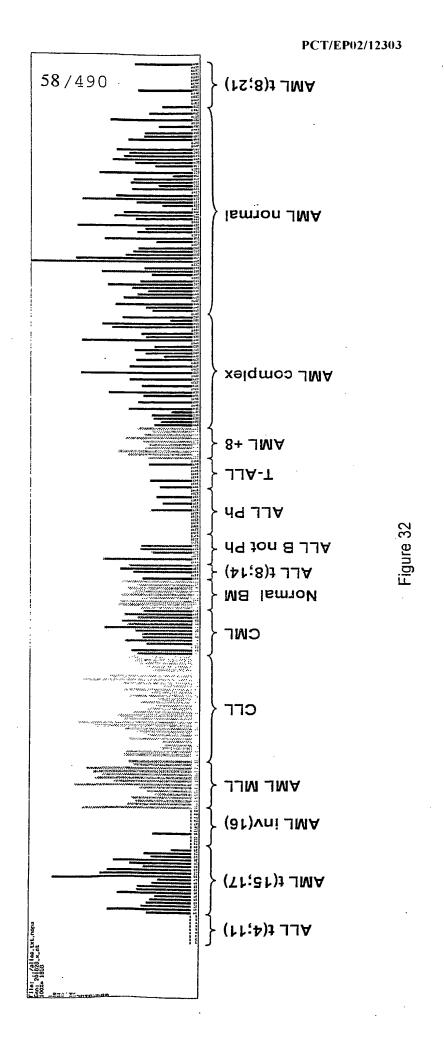
210045\_at, IDH2, ALL t(4;11) vs. CLI



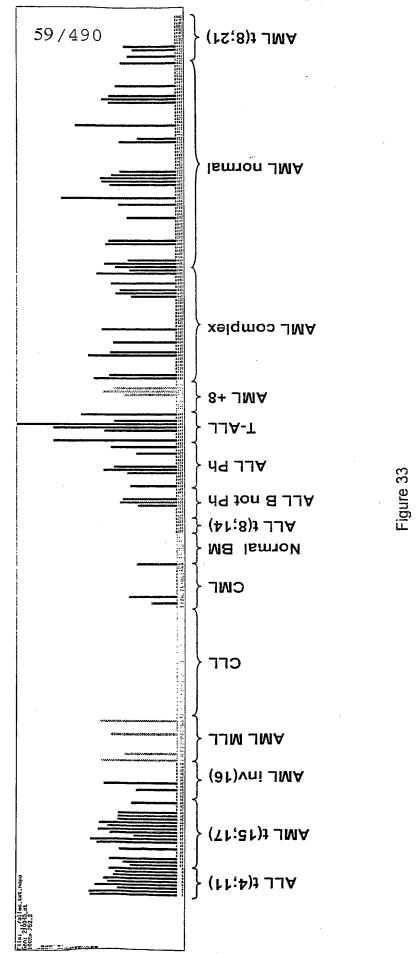
#### 221969\_at, PAX5, ALL t(4;11) vs. CM

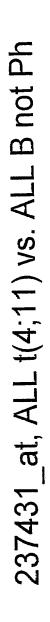


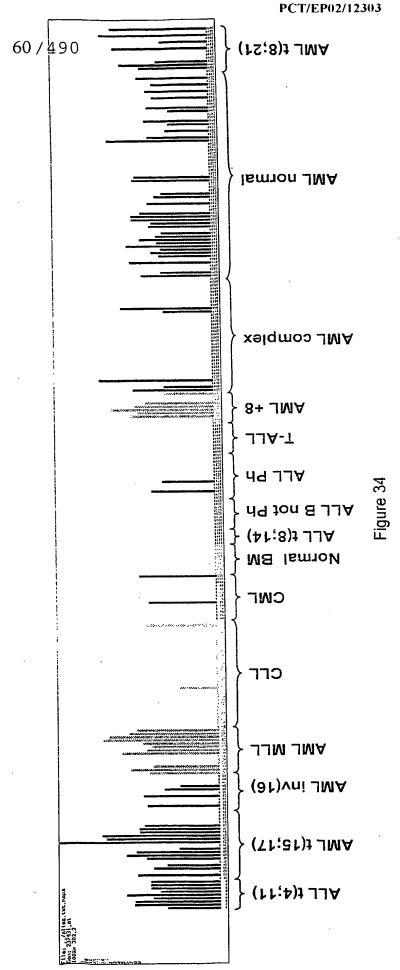
# 201828\_x\_at, CXX1, ALL t(4;11) vs. normal BM



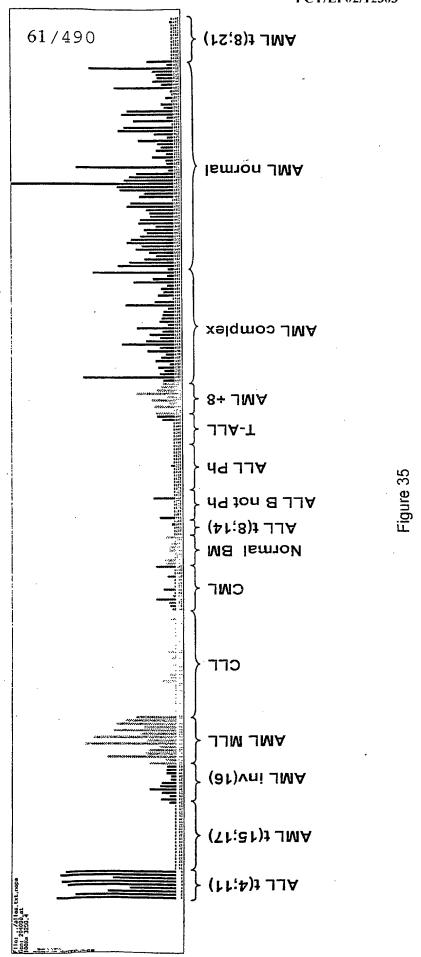
### 210045\_at, IDH2, ALL t(4;11) vs. ALL t(8;14)



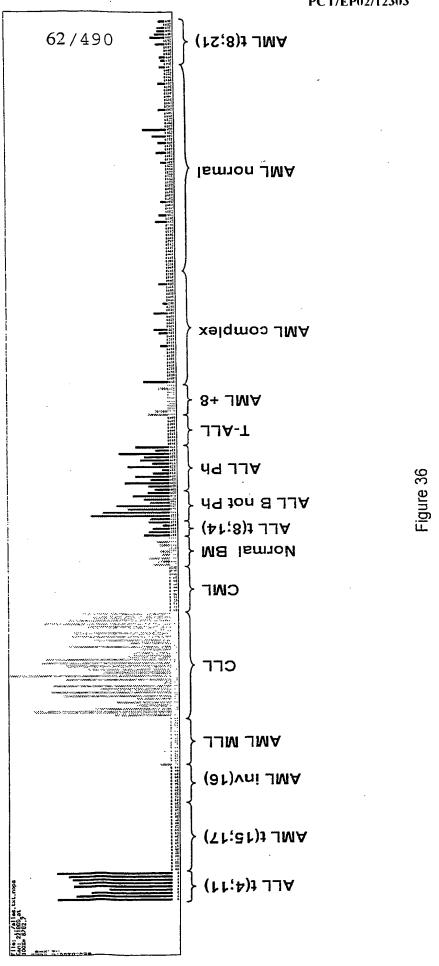




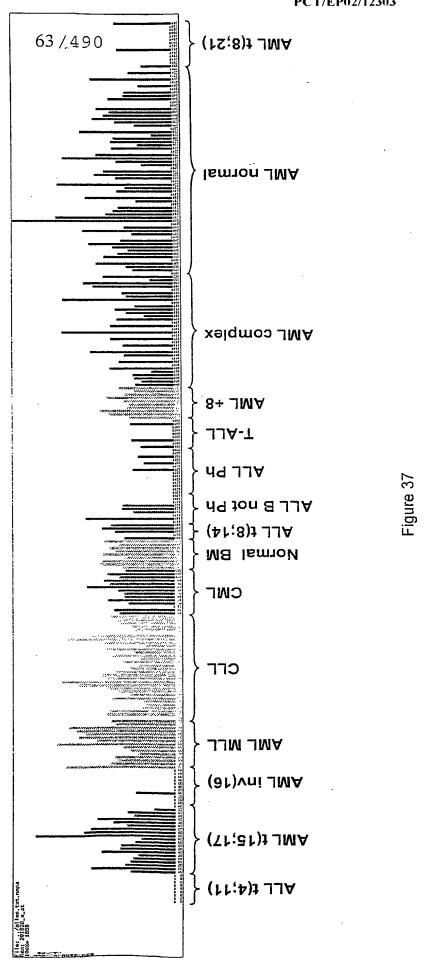
#### 204069\_at, MEIS1, ALL t(4;11) vs. ALL Ph

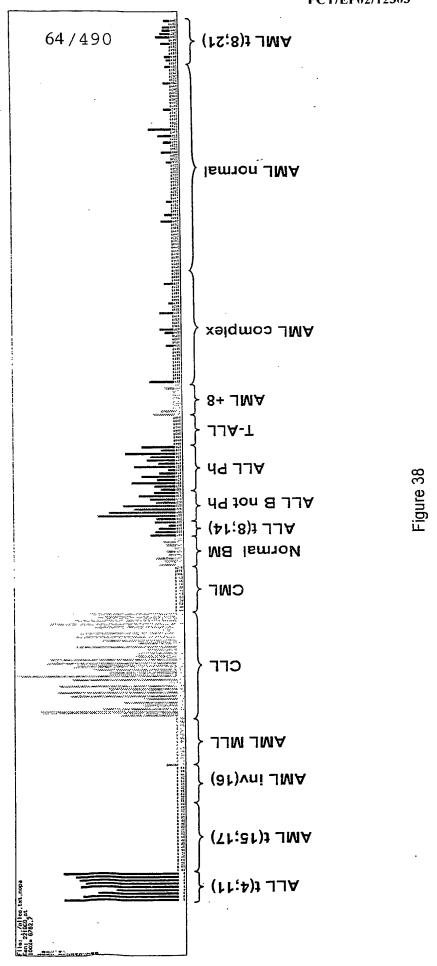


#### 221969\_at, PAX5, ALL t(4;11) vs. T-Al

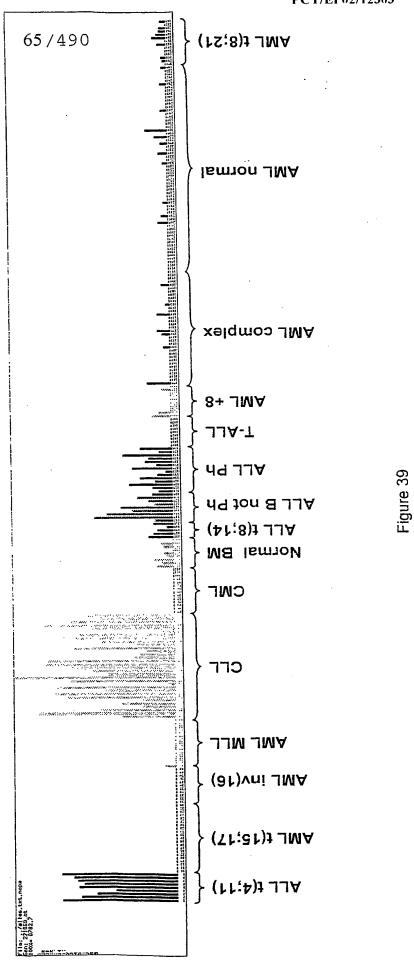


### 201828\_x\_at, CXX1, ALL t(4;11) vs. AML +8

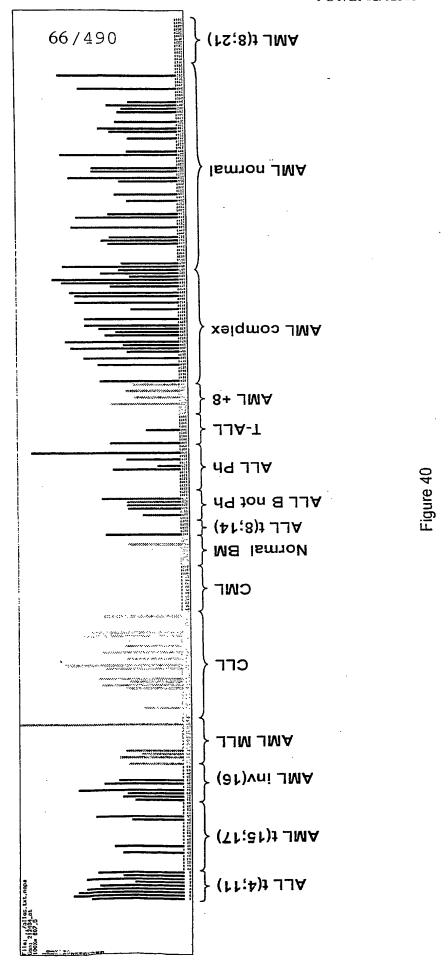




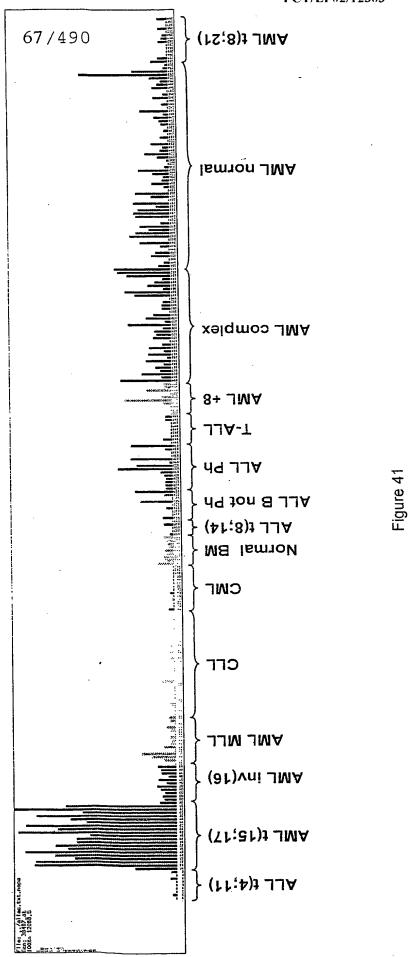
## 221969\_at, PAX5, ALL t(4;11) vs. AML normal



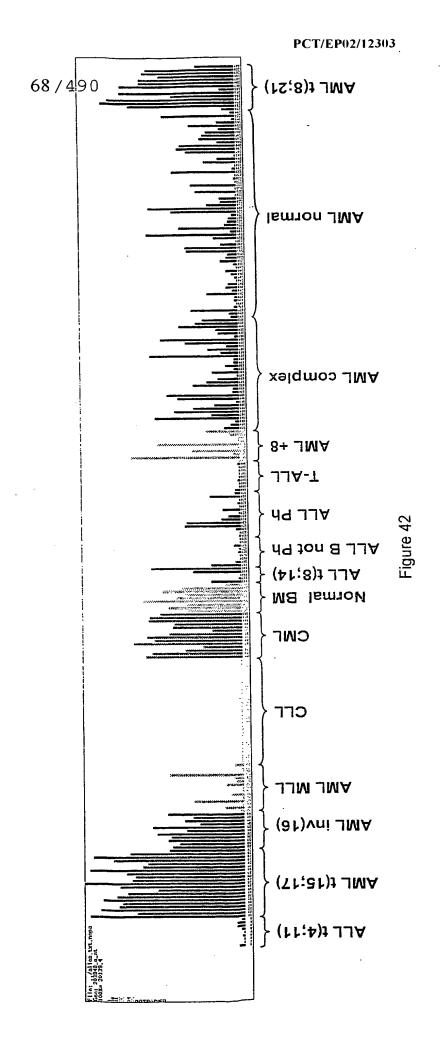
## 212484\_at, MTVR, ALL t(4;11) vs. AML t(8;21)



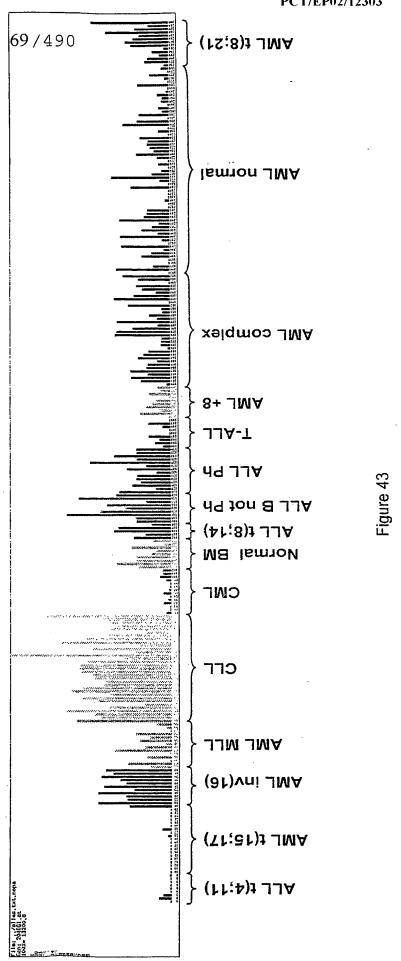
38487\_at, FLJ12442, AML t(15;17) vs. all others



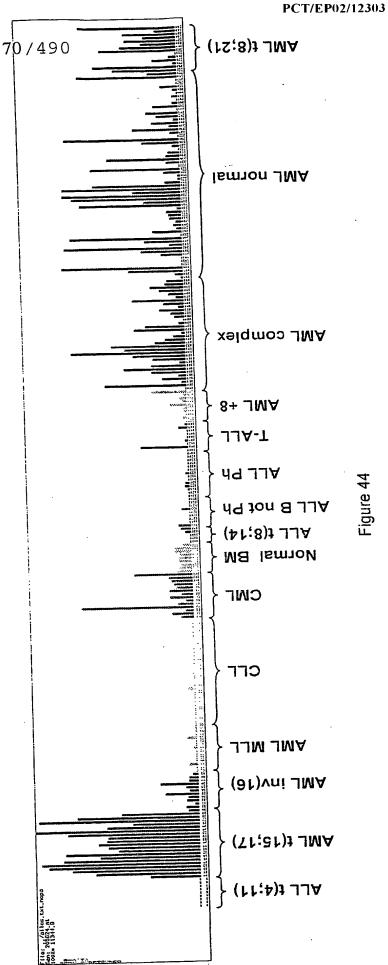
203948\_s\_at, MPO, AML t(15;17) vs. all others



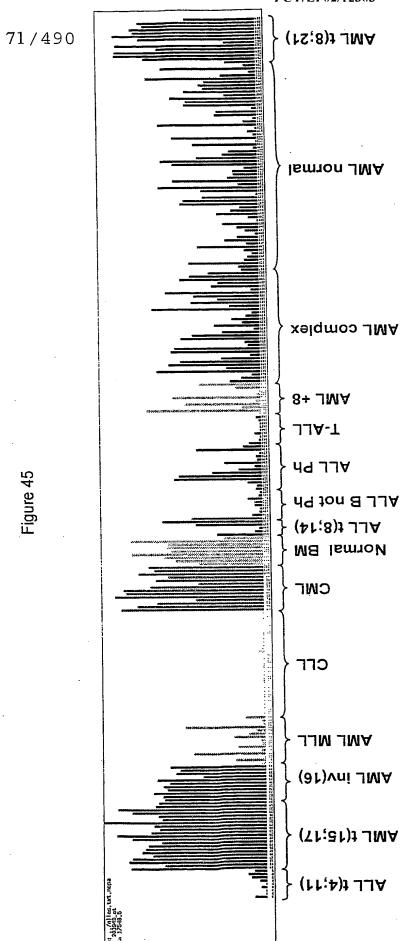
# 204661\_at, CDW52, AML t(15;17) vs. AML inv(16)

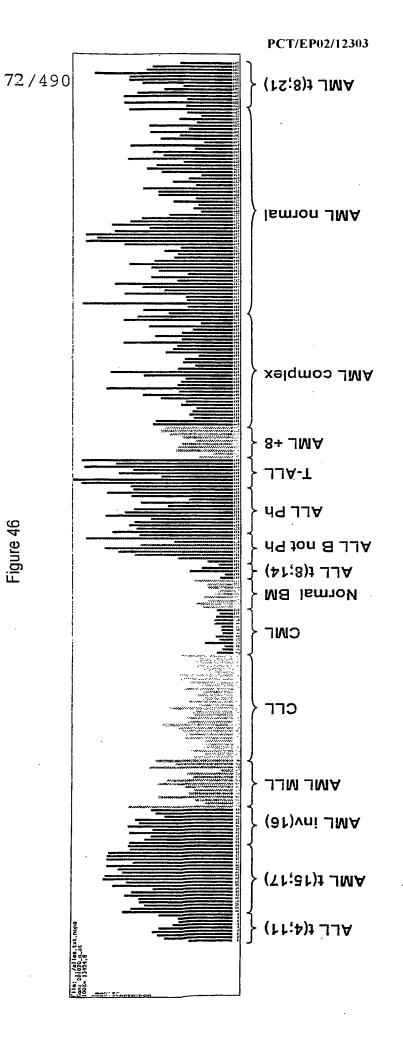


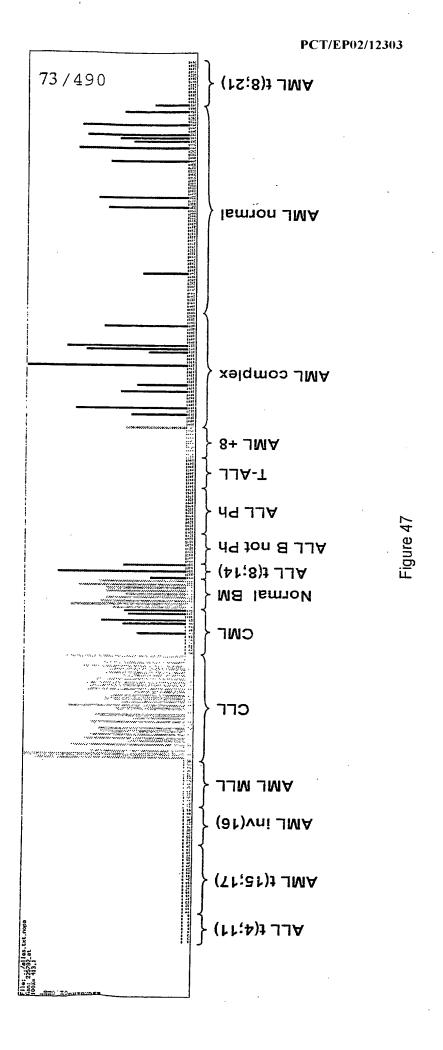
# 205624\_at, CPA3, AML t(15;17) vs. AML ML



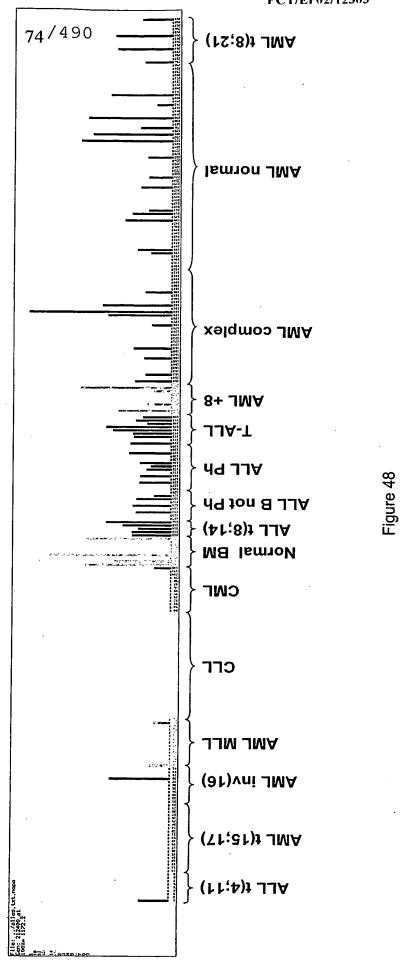


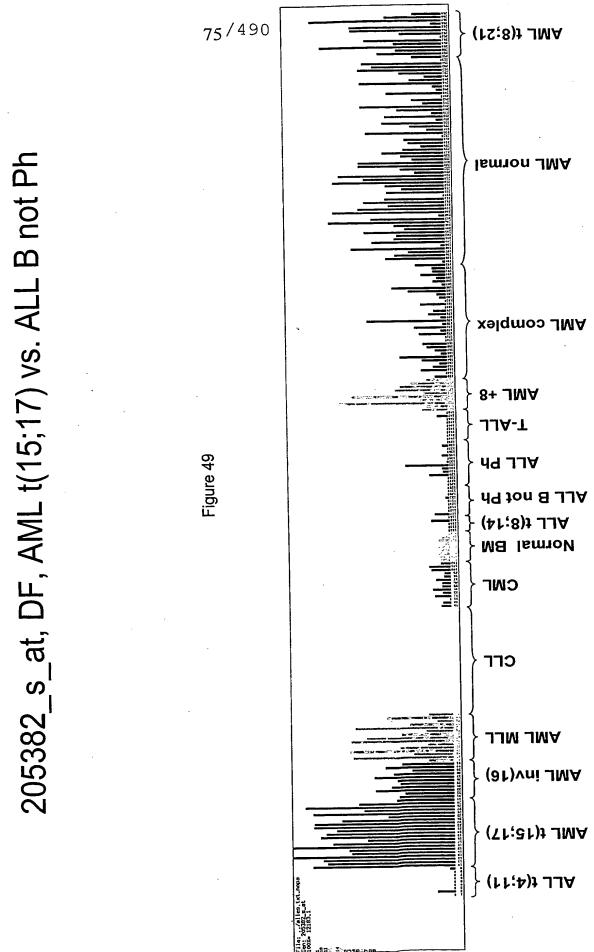


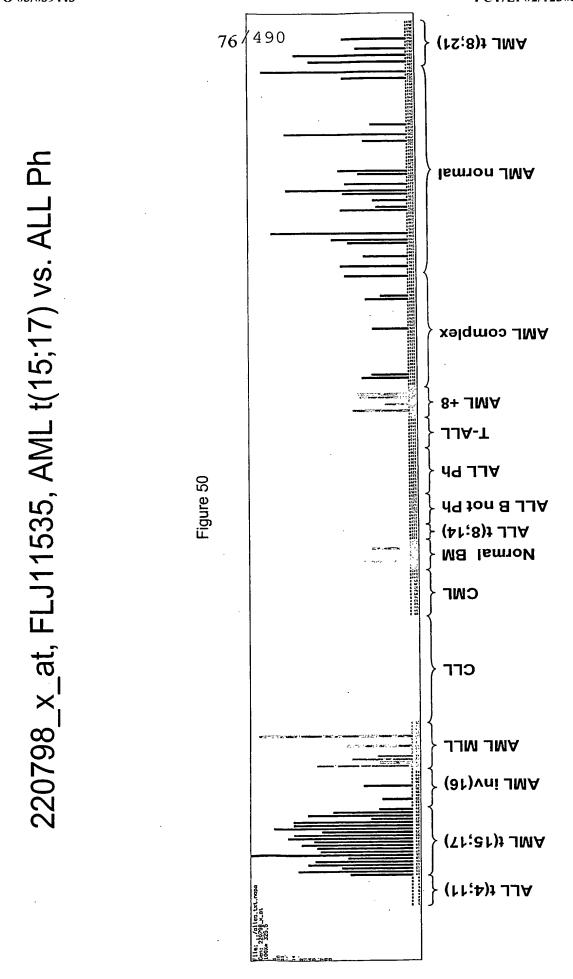








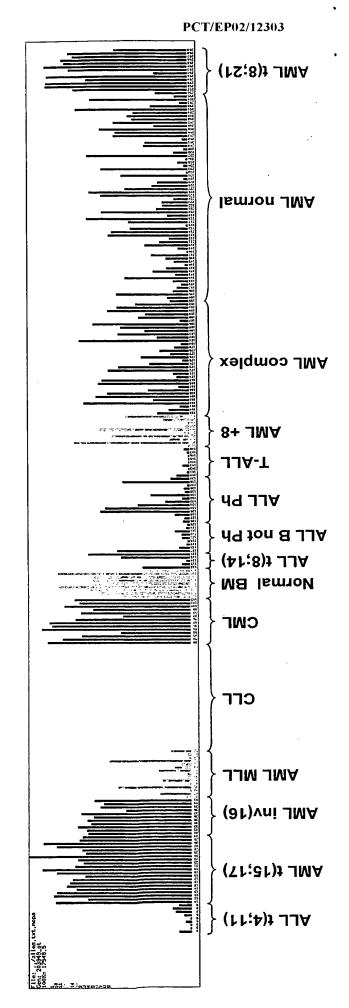




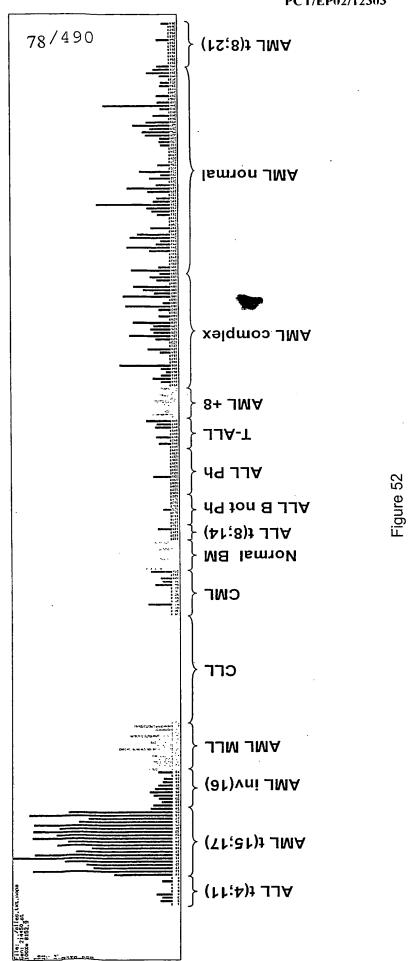
77/490

203949\_at, MPO, AML t(15;17) vs. T-ALI

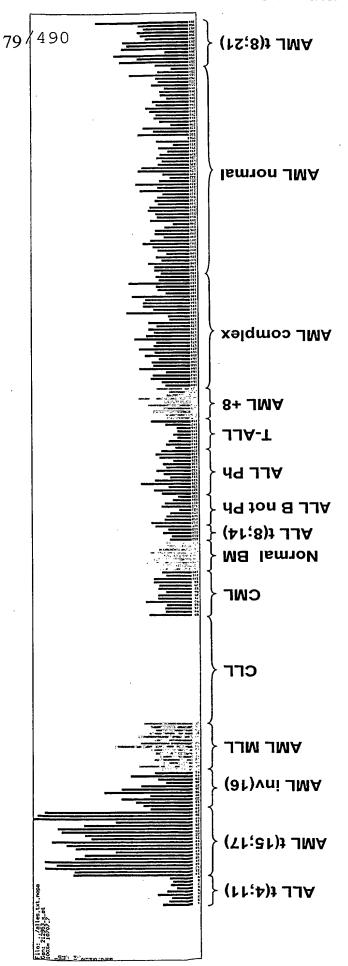
Figure 51



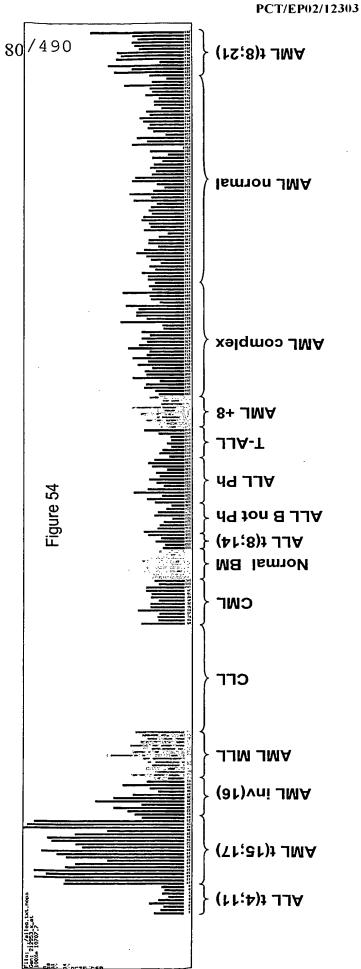
214450\_at, CTSW, AML t(15;17) vs. AML +8



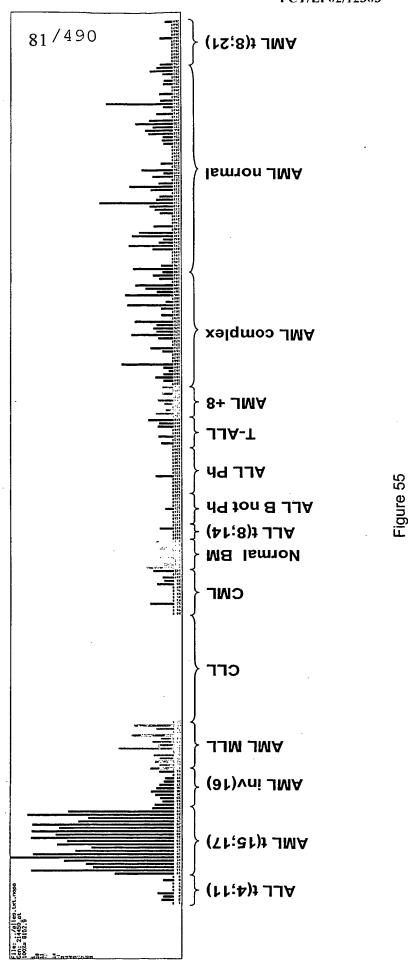
212953\_x\_at, CALR, AML t(15;17) vs. AML complex



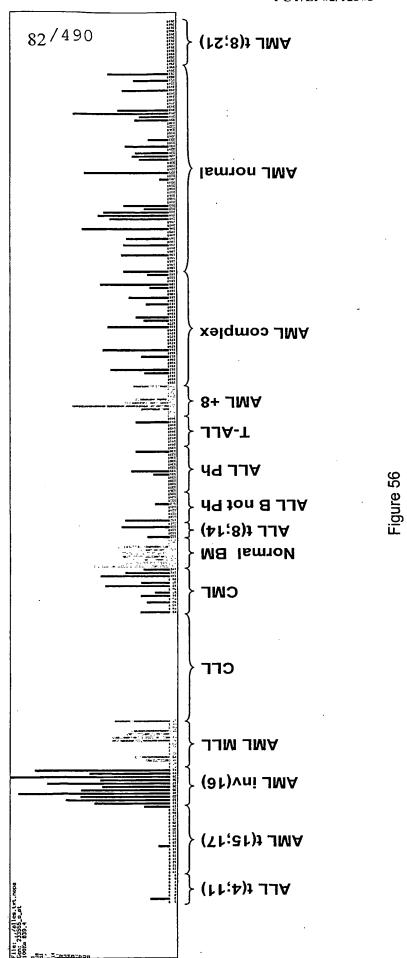
212953\_x\_at, CALR, AML t(15;17) vs. AML normal



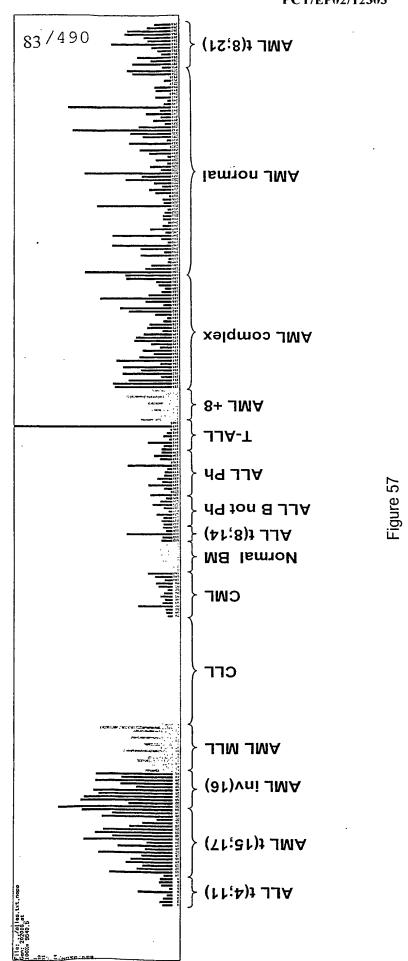
214450\_at, CTSW, AML t(15;17) vs. AML t(8;21)



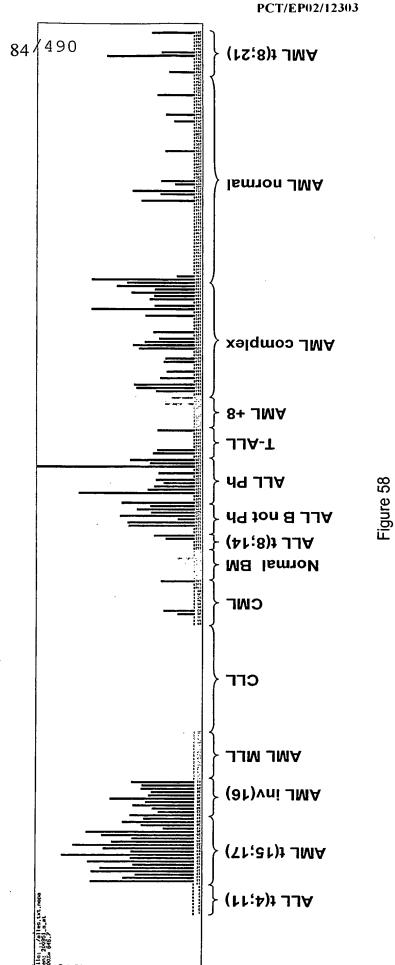
233555\_s\_at, AML inv(16) vs. all others



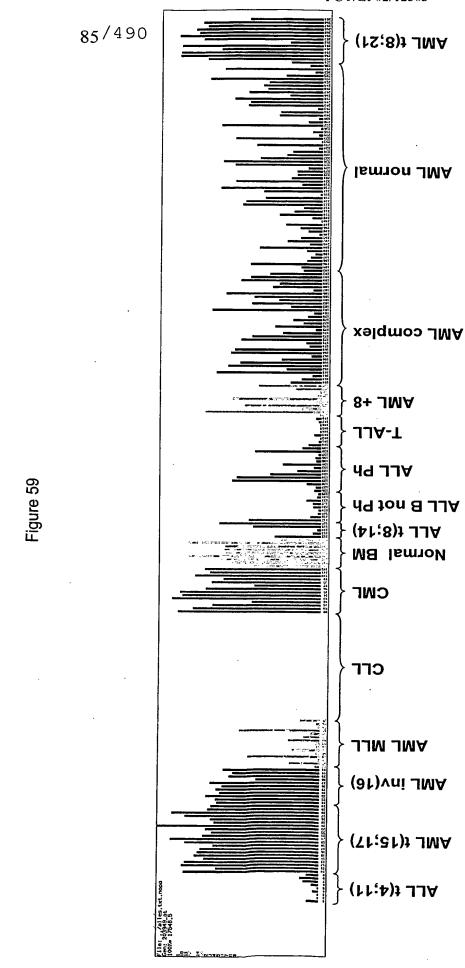
202016\_at, MEST, AML inv(16) vs. all others











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Figure 60

225792\_at, AML inv(16) vs. normales KM

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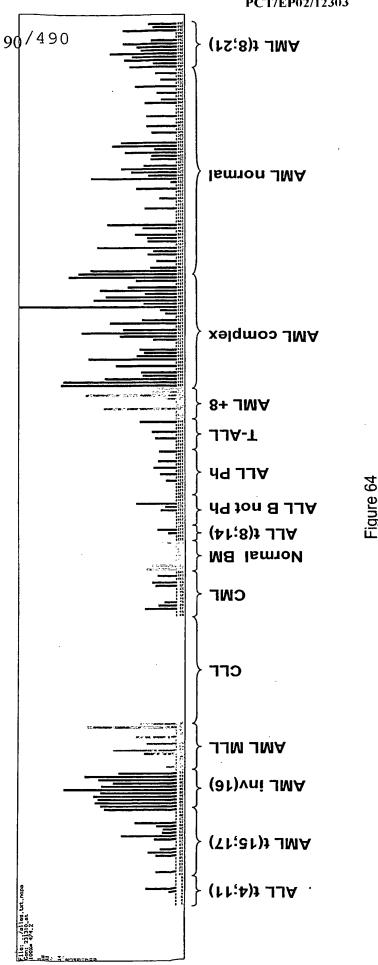
214558\_at, GPR12, AML inv(16) vs. ALL t(8;14) Figure 62

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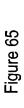


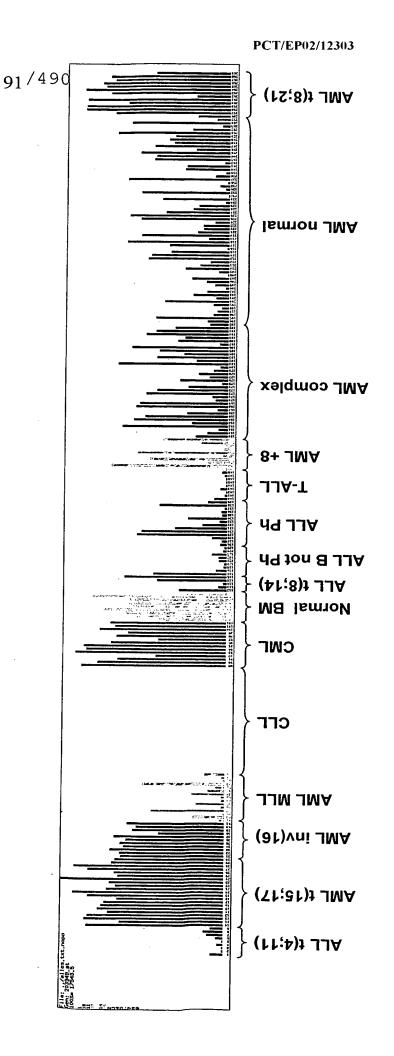
Figure 63

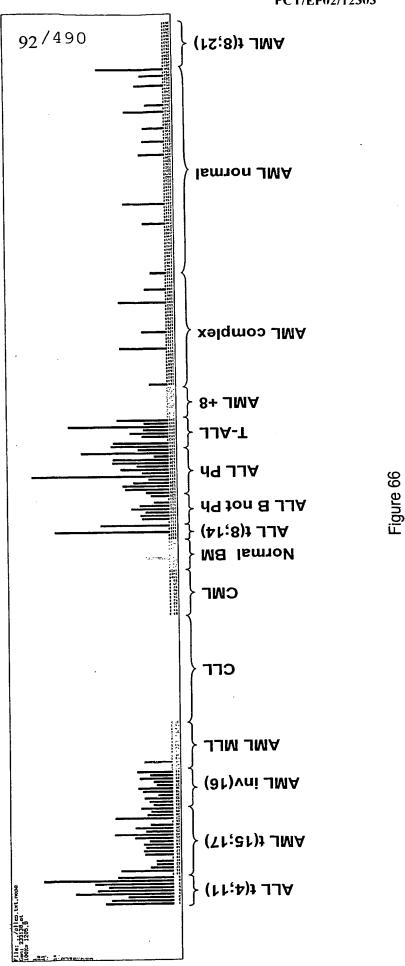
231310\_at, AML inv(16) vs. ALL Ph



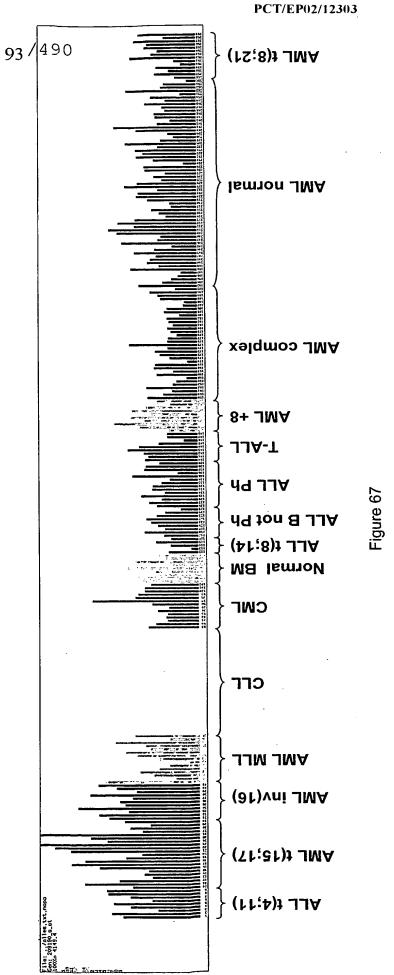
#### 203949\_at, MPO, AML inv(16) vs. T-ALI

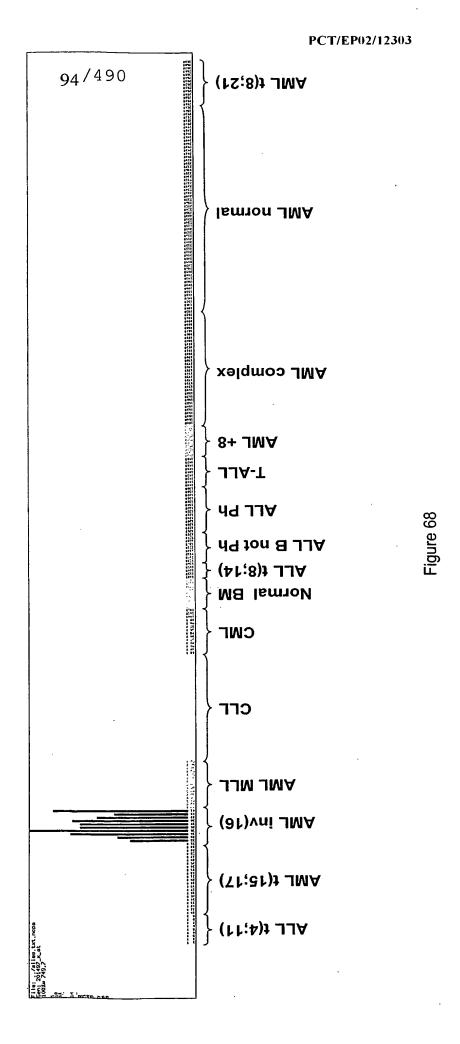




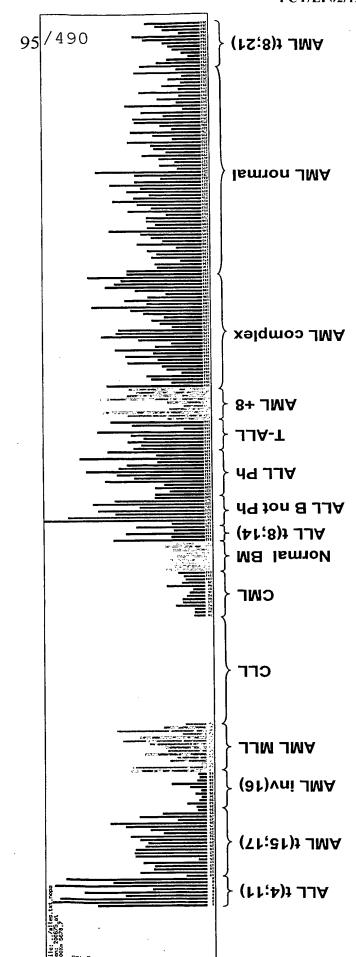




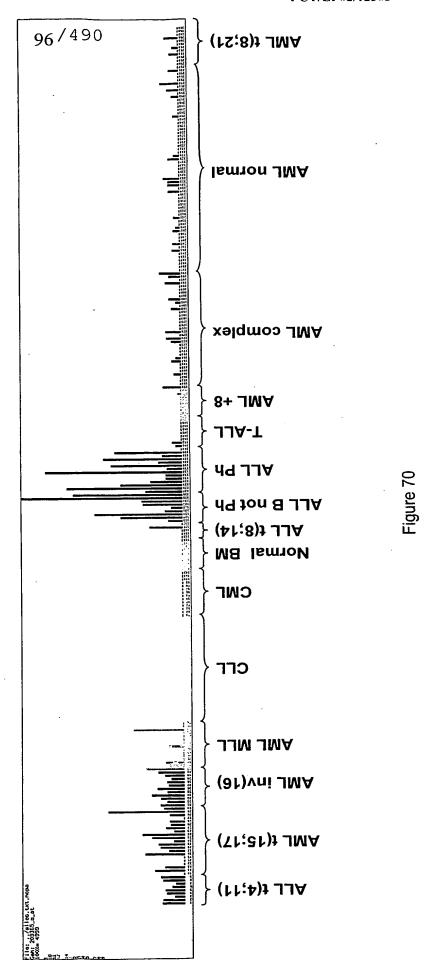




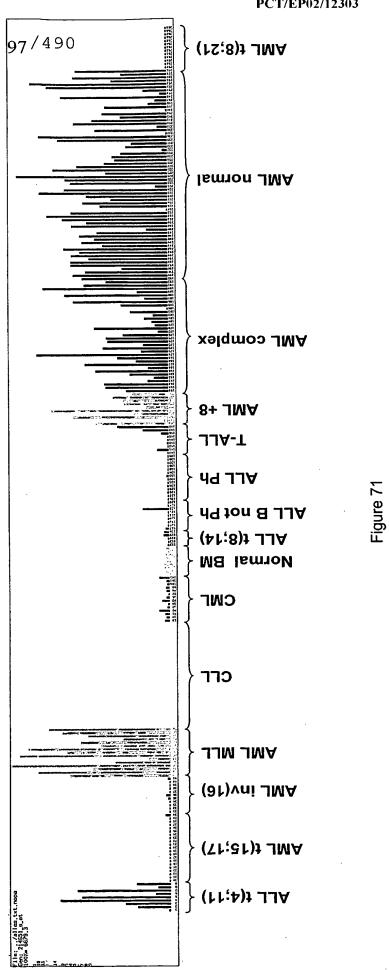
200675\_at, CD81, AML inv(16) vs. AML complex



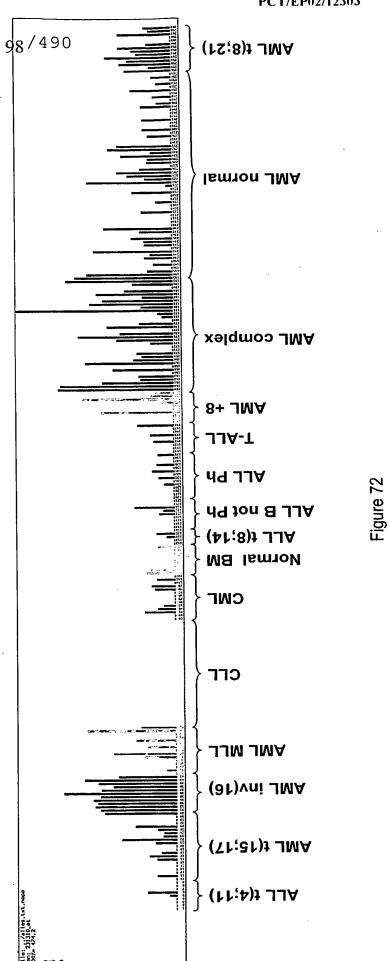
## 209365\_s\_at, ECM1, AML inv(16) vs. AML norma



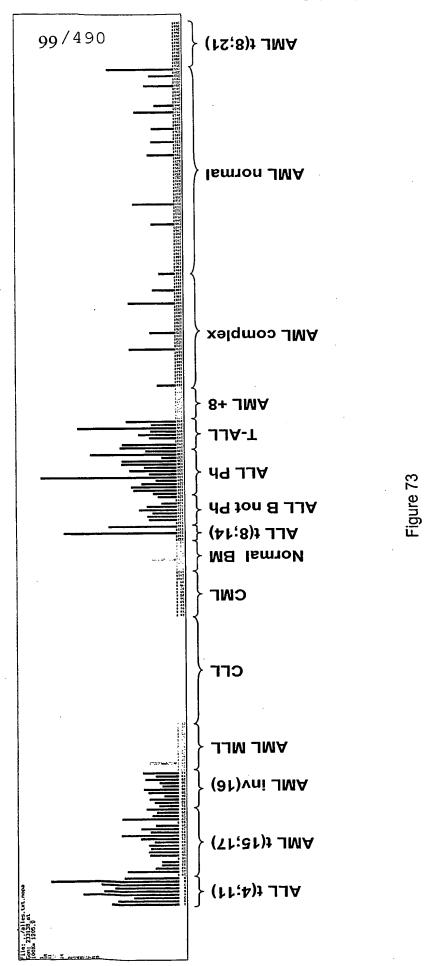
214641\_s\_at, HOXA9, AML inv(16) vs. AML normal



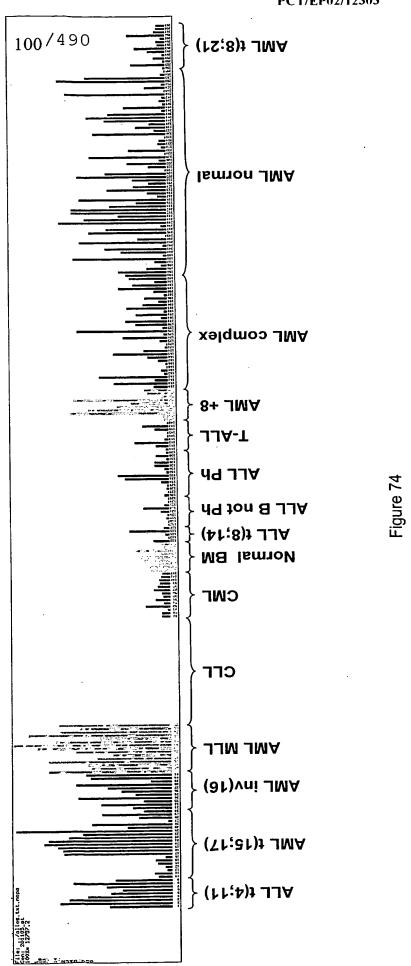




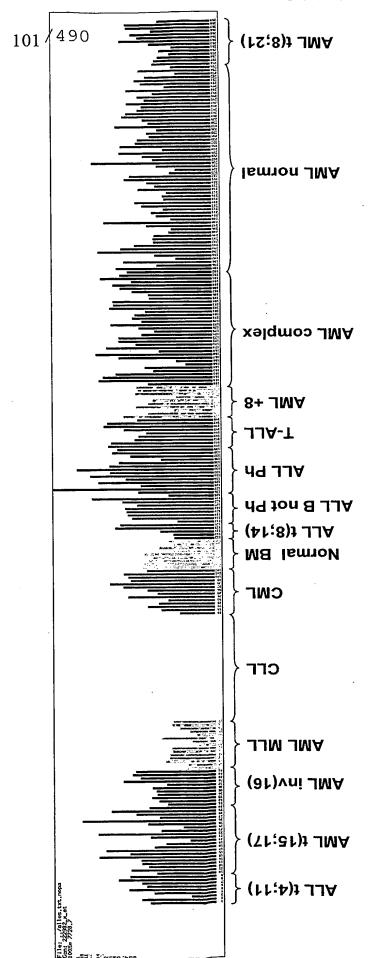
233138\_at, AML inv(16) vs. AML t(8;21)



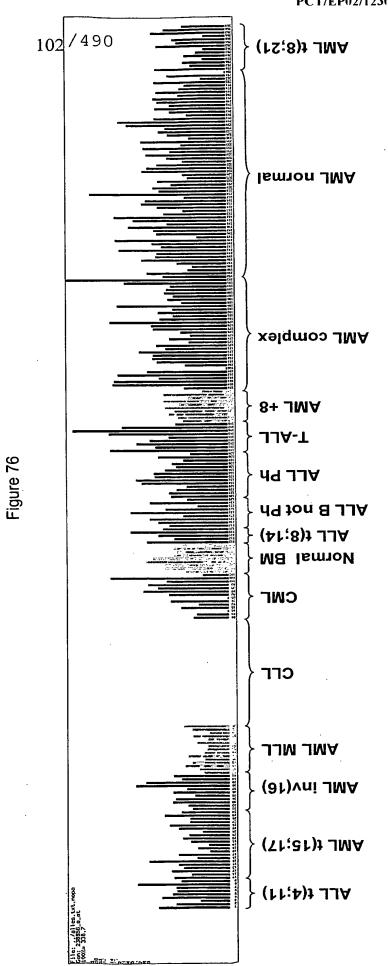
201105\_at, LGALS1, AML MLL vs. all others



222982\_x\_at, SLC38A2, AML MLL vs. all others

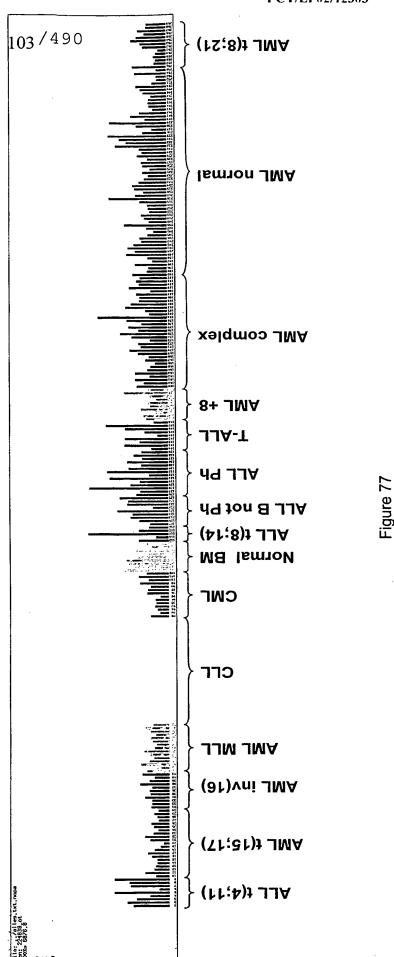


238856\_s\_at, AML MLL vs. all others

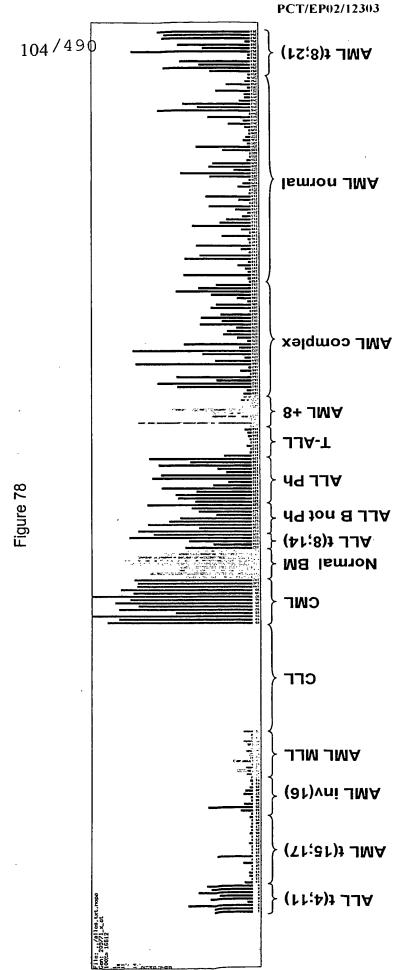


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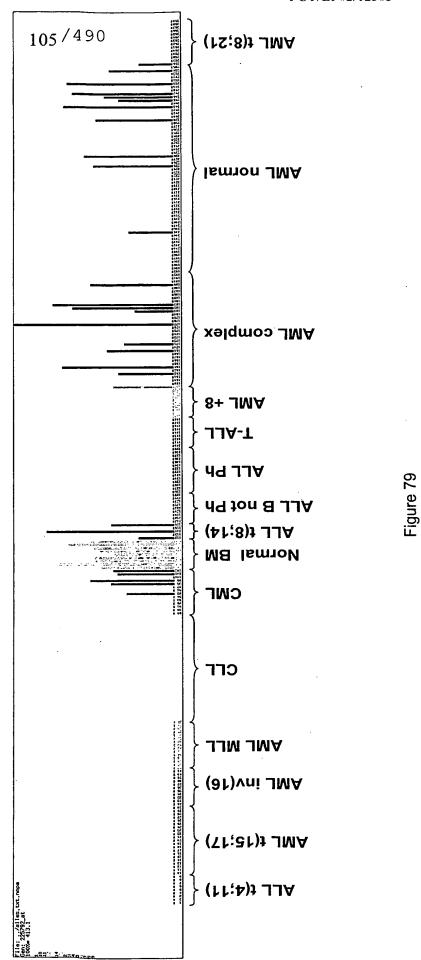
224838\_at, AML MLL vs. CLL

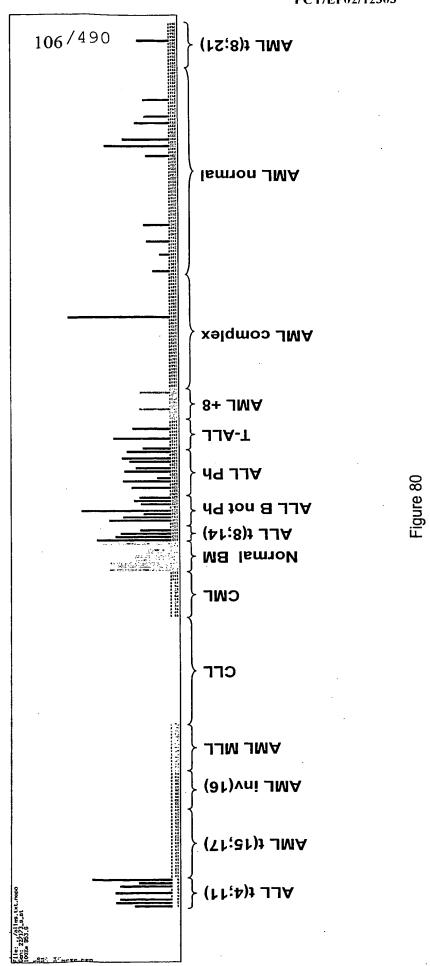


209771\_x\_at, CD24, AML MLL vs. CMI

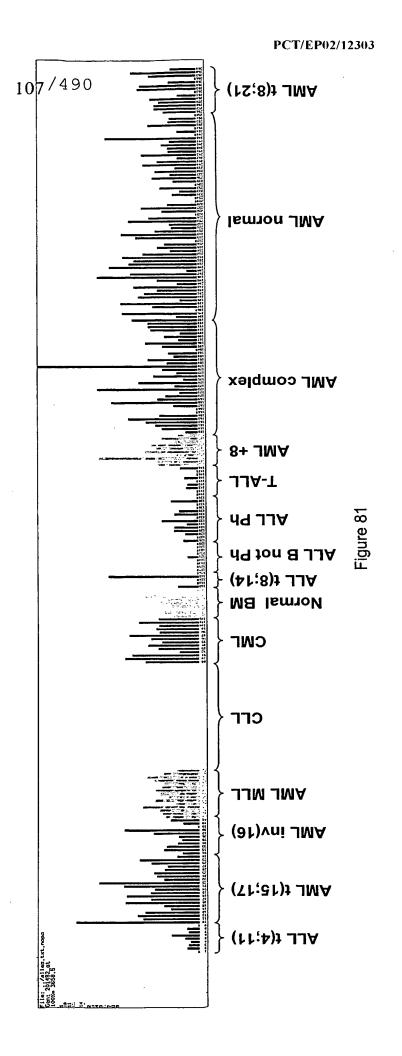


225792\_at, AML MLL vs. normal BM

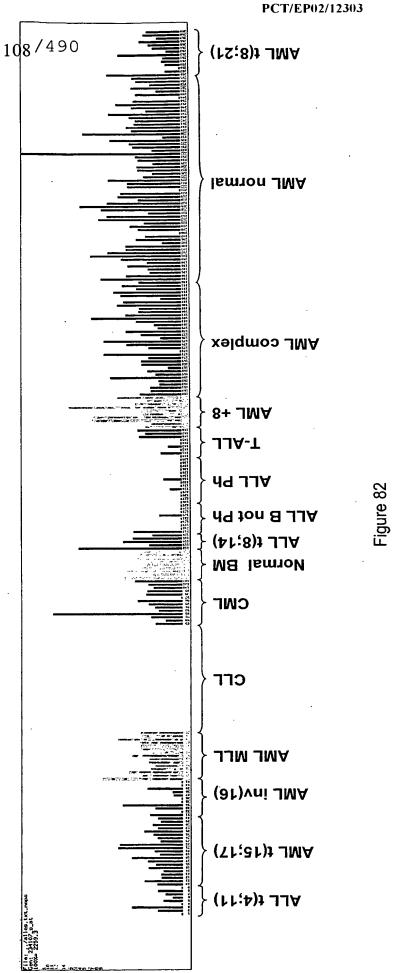




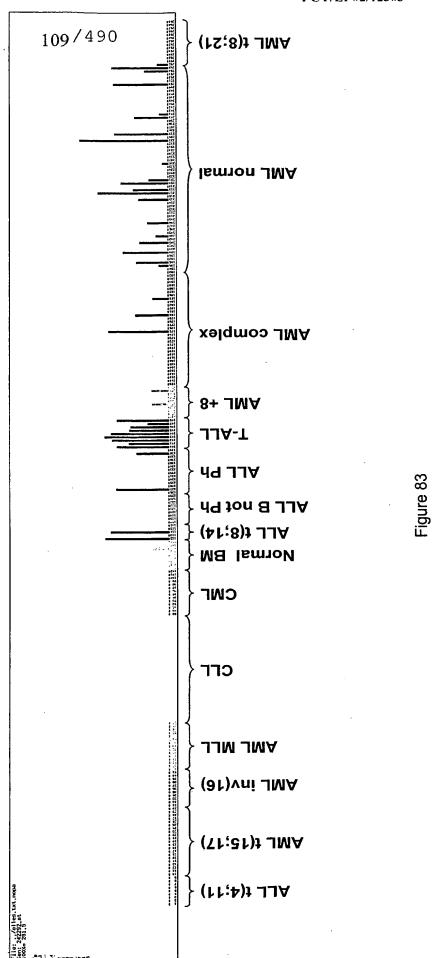
201482\_at, QSCN6, AML MLL vs. ALL B not Ph



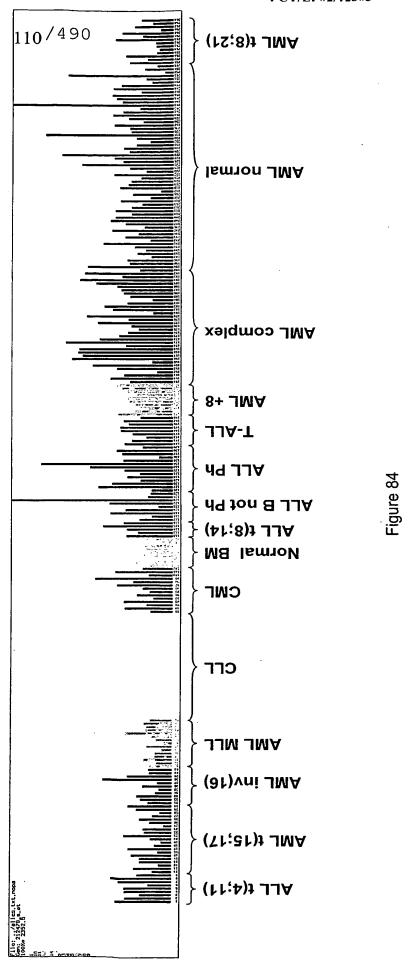
234107\_s\_at, AML MLL vs. ALL Ph



242292\_at, AML MLL vs. T-ALL



212479\_s\_at, FLJ13910, AML MLL vs. AML +8



218172\_s\_at, PRO2577, AML MLL vs. AML +8

(12;8)1 JMA

Ismnon JMA

CLL

AML MLL

(81)vni JMA

(Tr;31)1 JMA

\r\;4)1 \\

| CML | CML

111/490

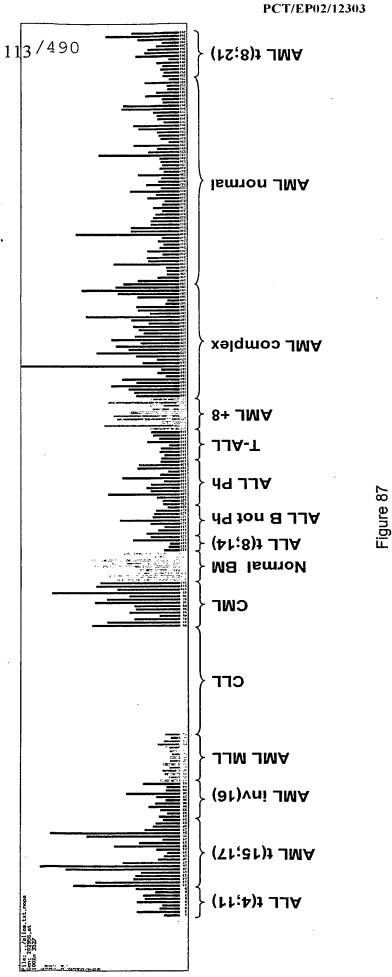
igure 85

200867\_at, AML MLL vs. AML +8

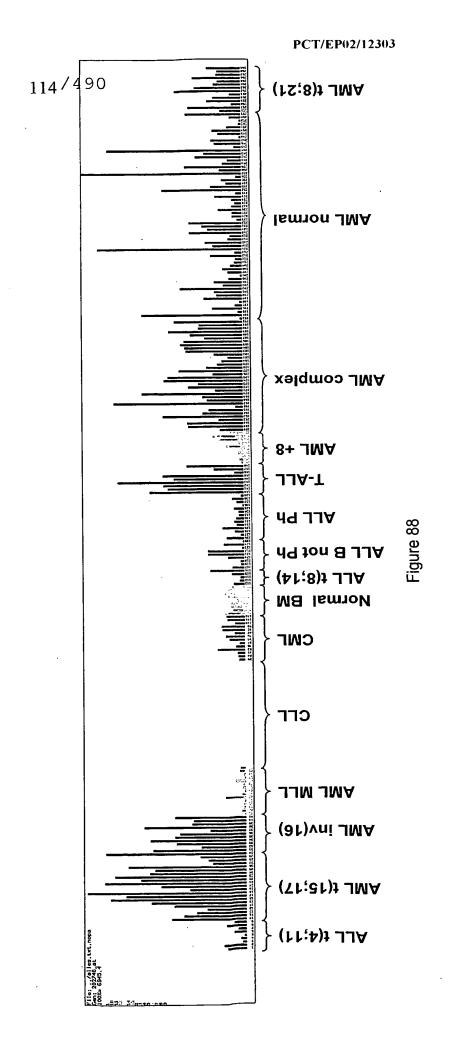
WO 03/039443

Figure 86

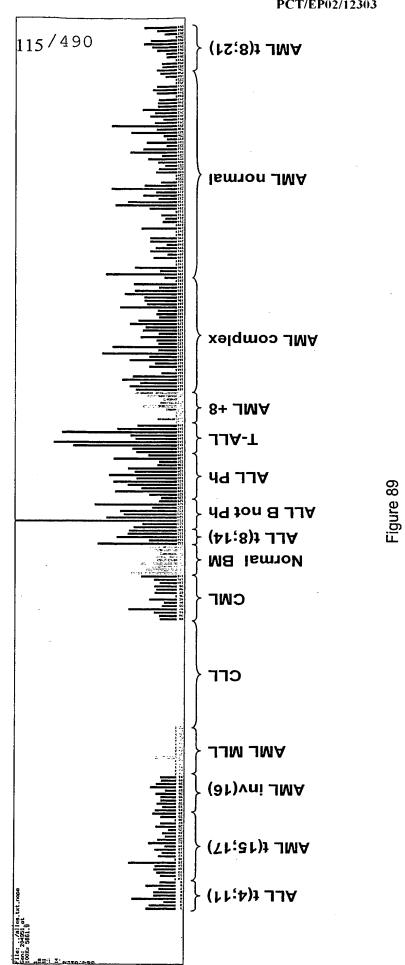
202956\_at, BIG1, AML MLL vs. AML +8



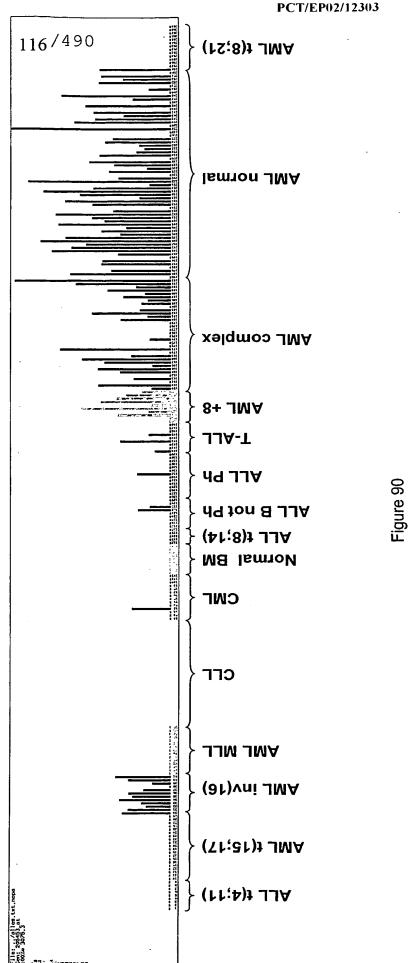
202746\_at, AML MLL vs. AML complex



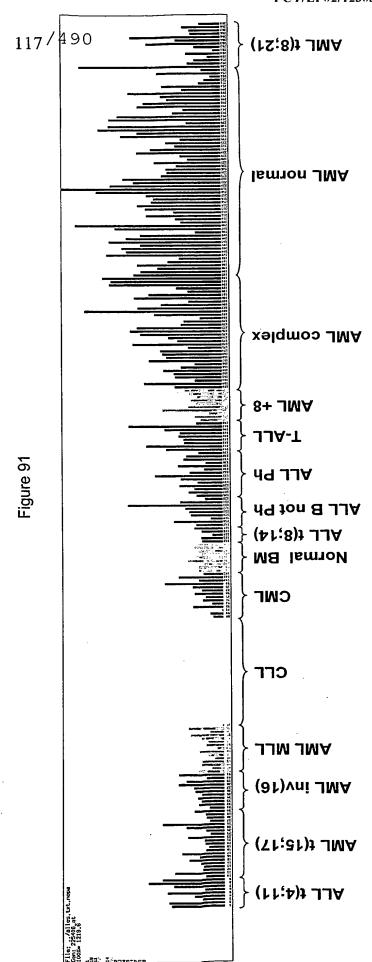
204951\_at, ARHH, AML MLL vs. AML complex



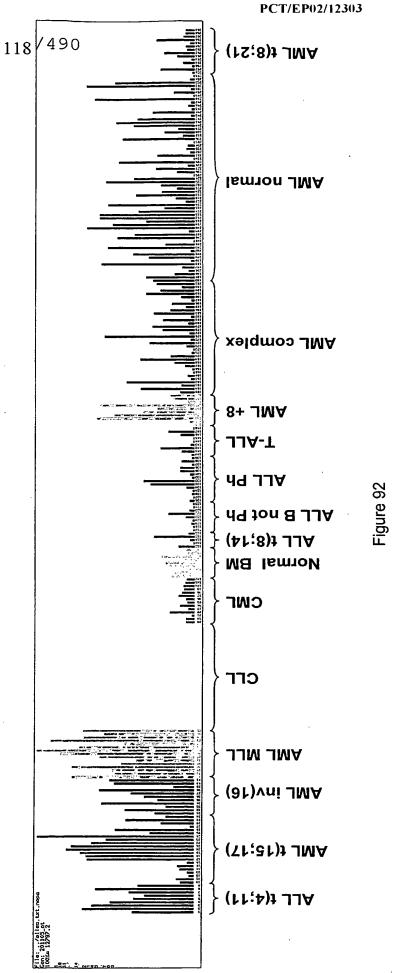
205453\_at, HOXB2, AML MLL vs. AML normal



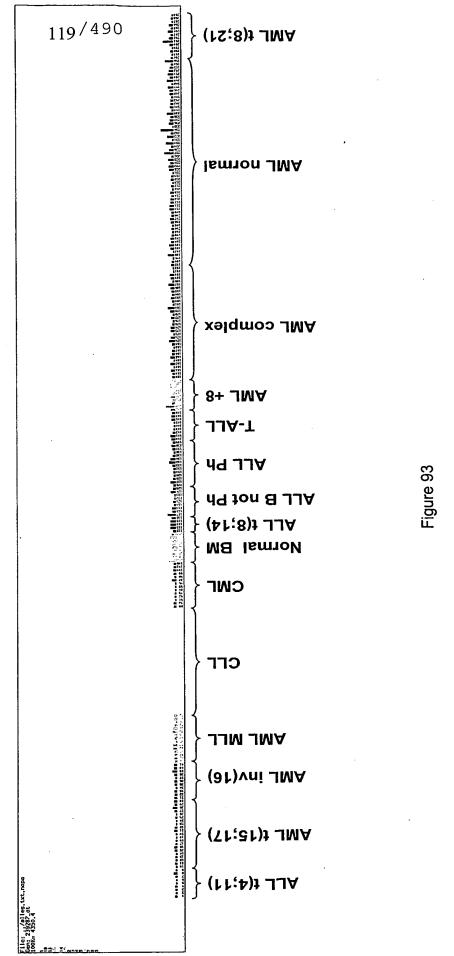
225406\_at, TSG, AML MLL vs. AML normal



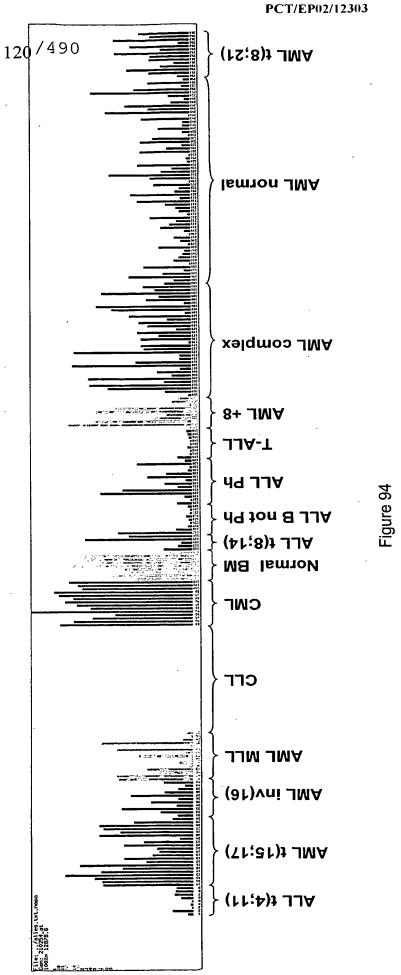




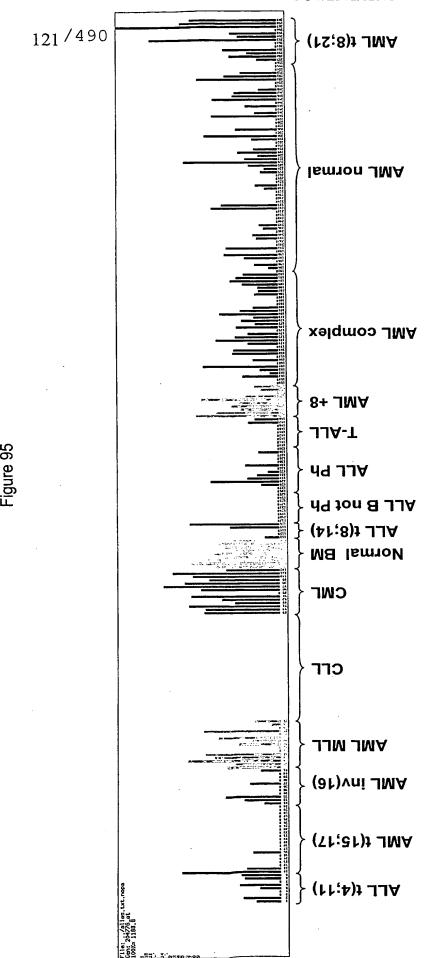
## 239287\_at, CLL vs. all others



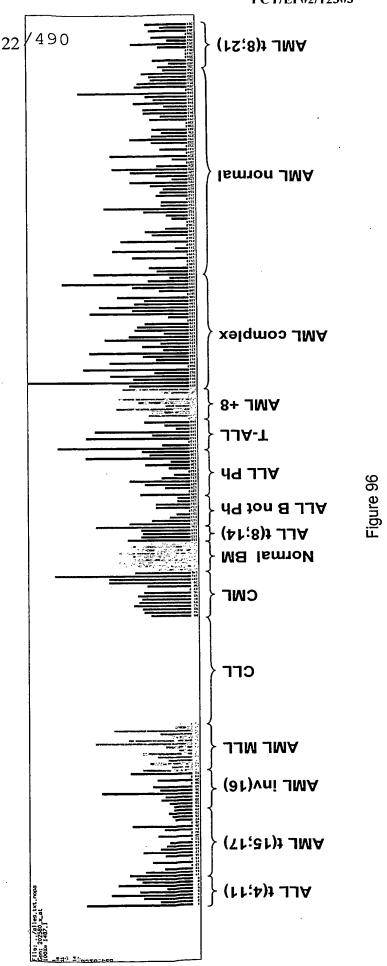
210254\_at, CLL vs. CMI



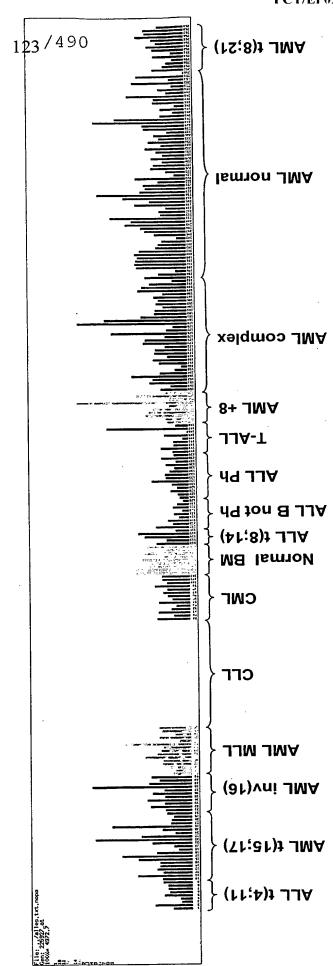




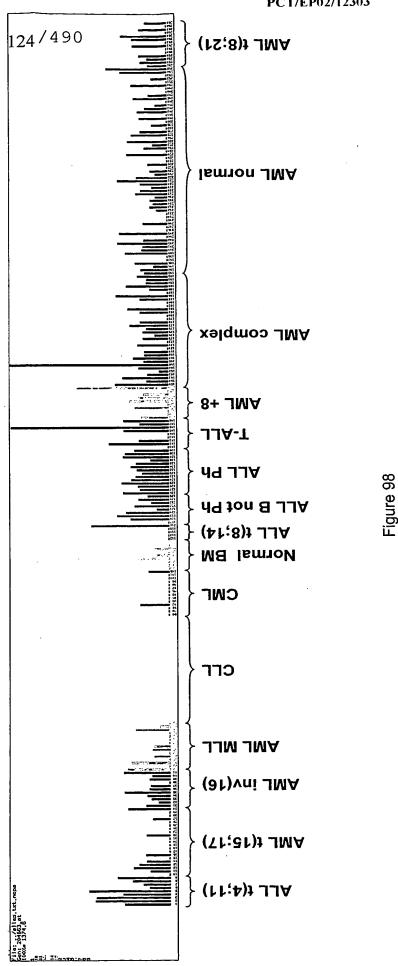




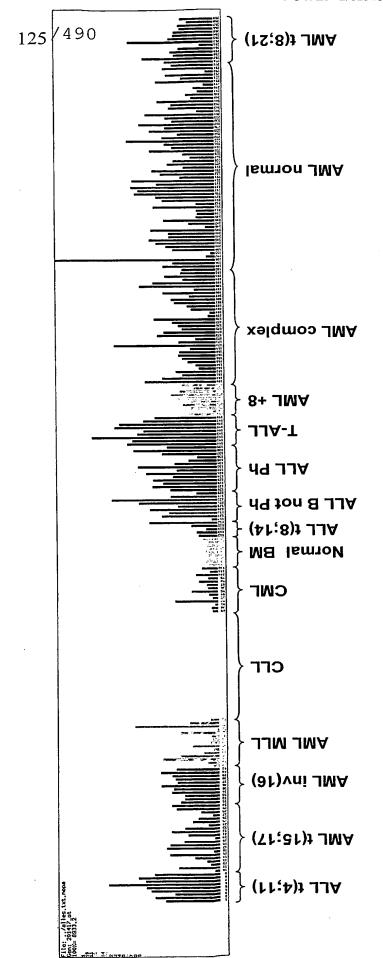
## 225927\_at, MAP3K1, CLL vs. ALL B not Ph



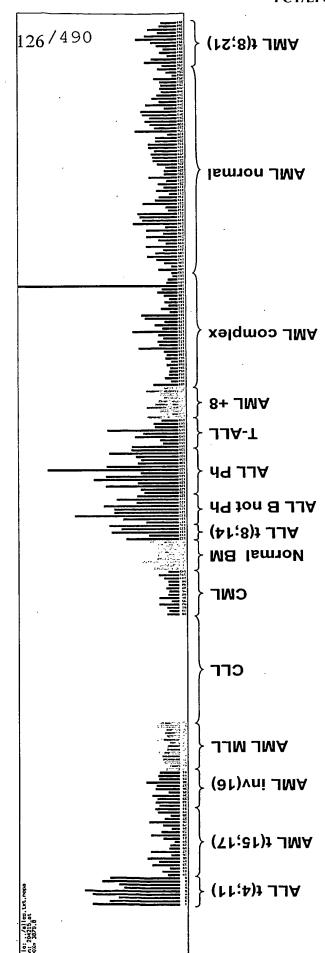
204663\_at, ME3, CLL vs. ALL Ph



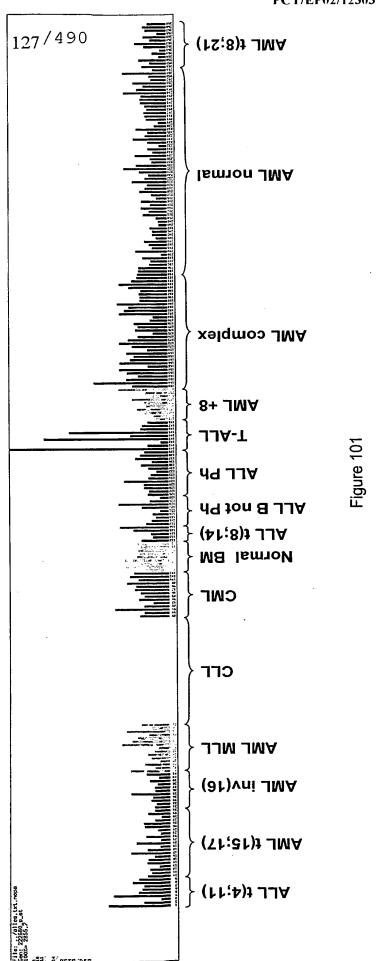




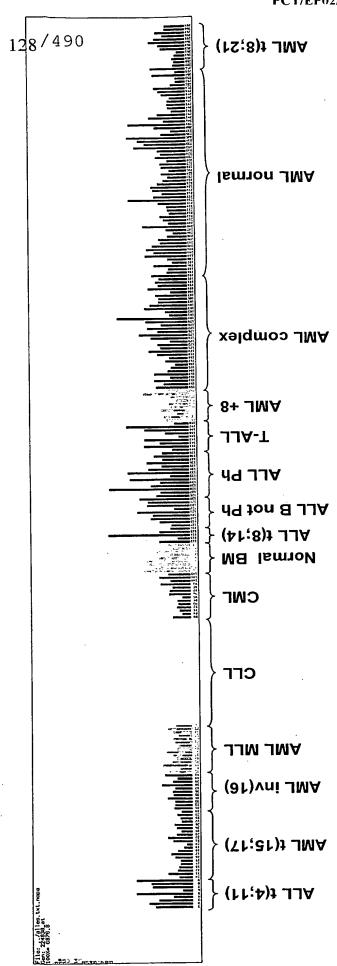
## 204215\_at, MGC4175, CLL vs. AML +8



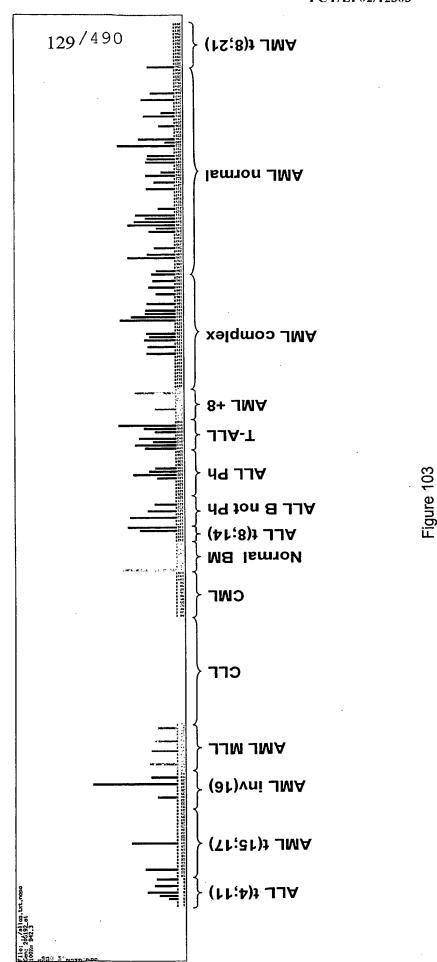
222680\_s\_at, RAMP, CLL vs. AML complex



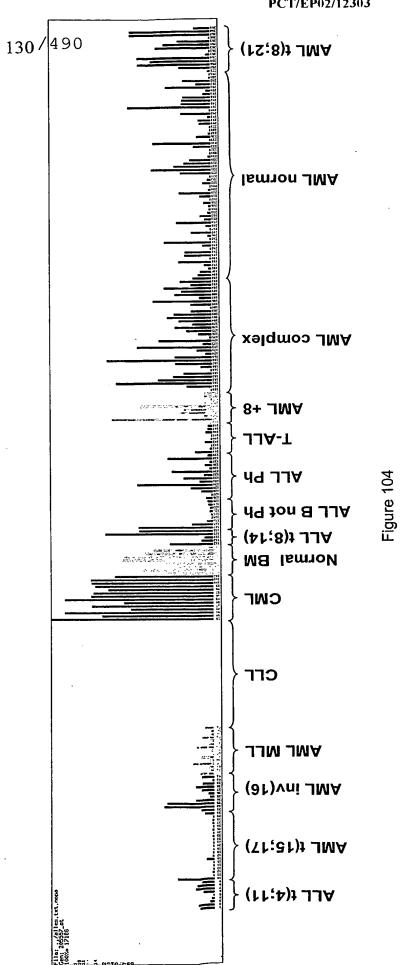




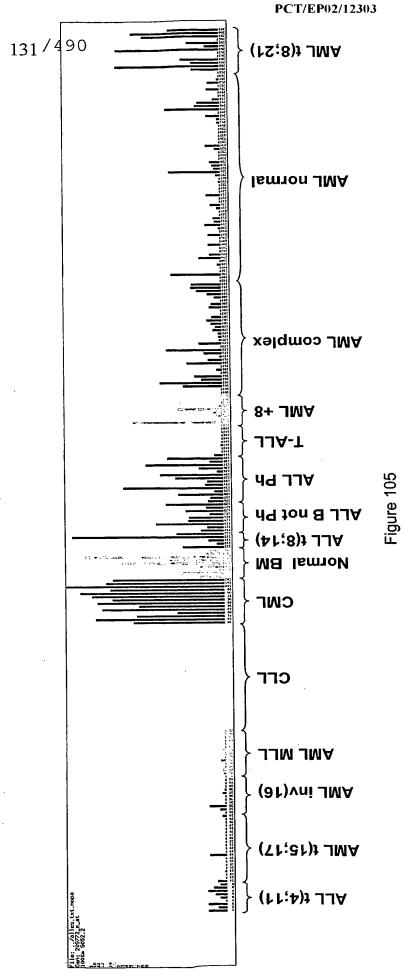
## 205192\_at, MAP3K14, CLL vs. AML t(8;21)



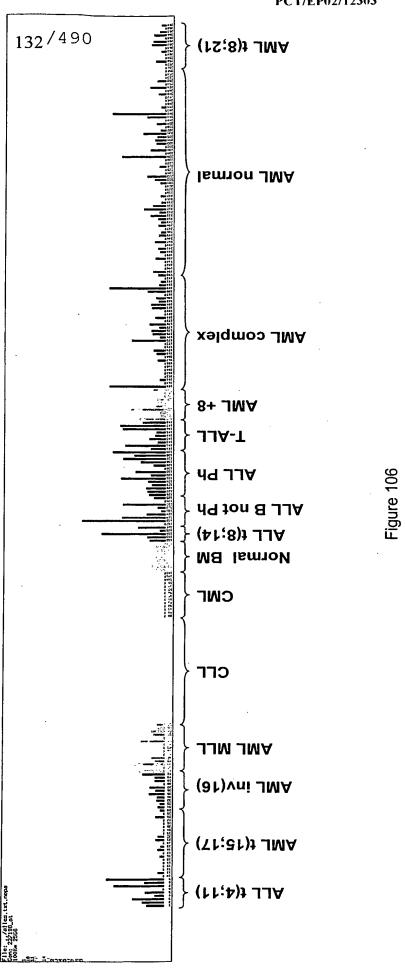


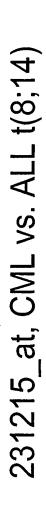


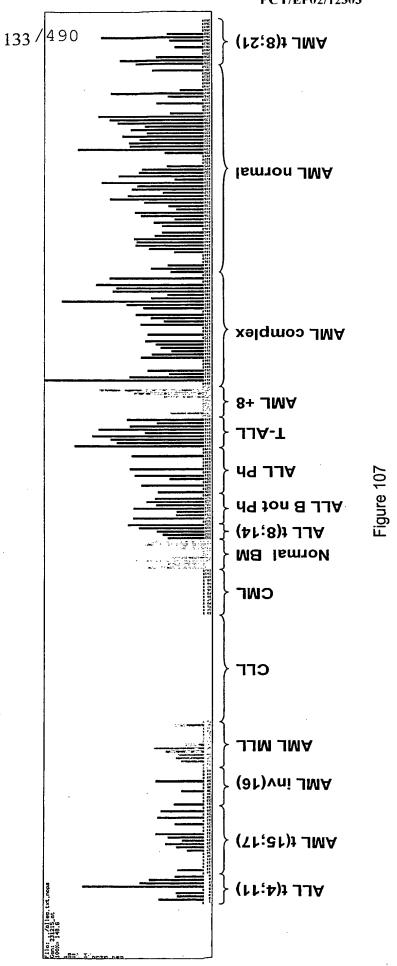
209772\_s\_at, CD24, CML vs. all others



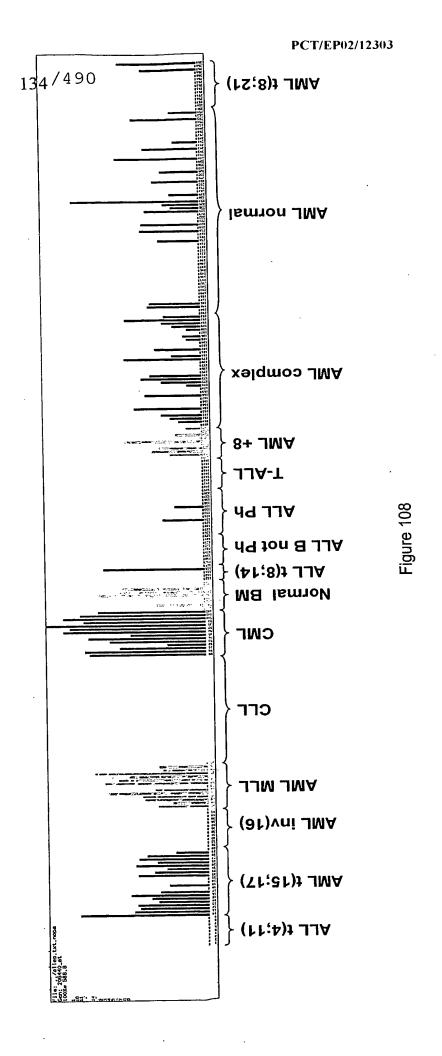
## 227198\_at, CML vs. normal BM

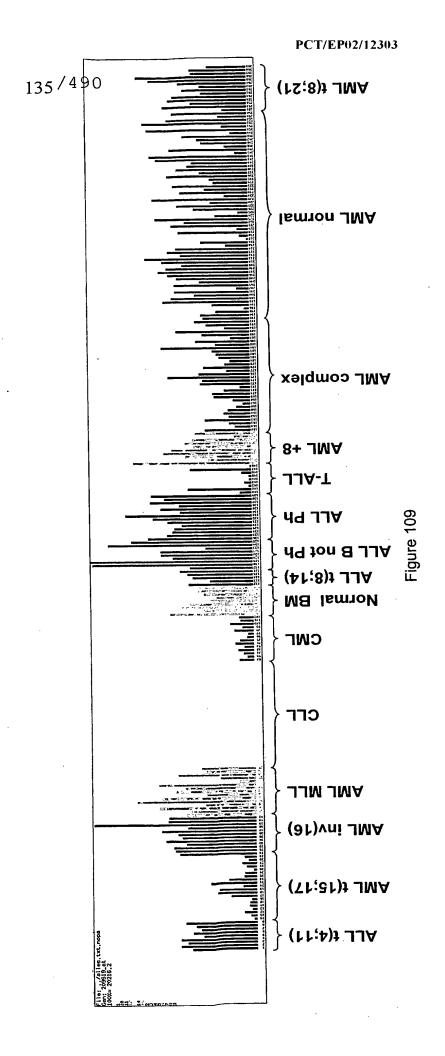




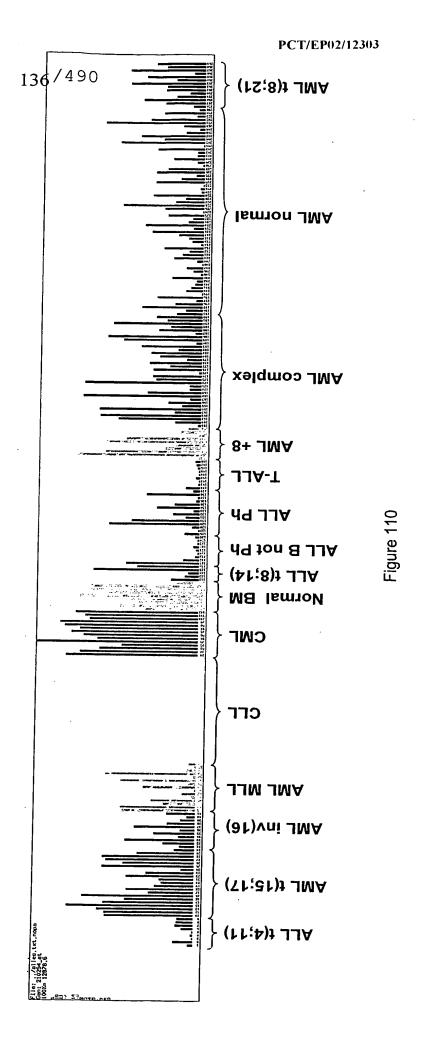


206440\_at, VELI1, CML vs. ALL B not Ph

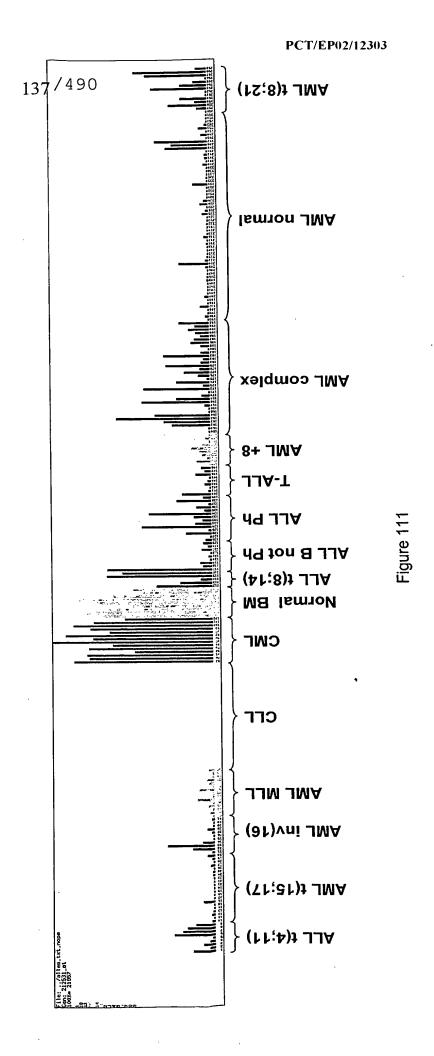




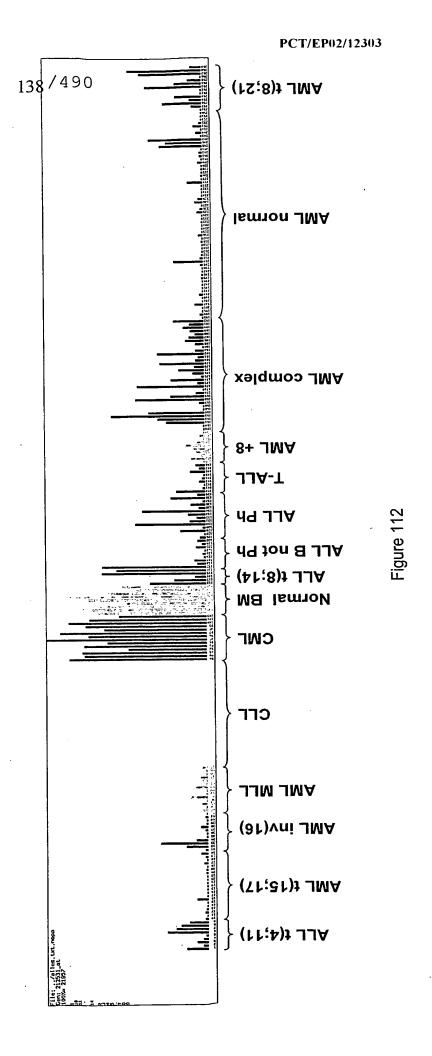
210254\_at, CML vs. T-ALL



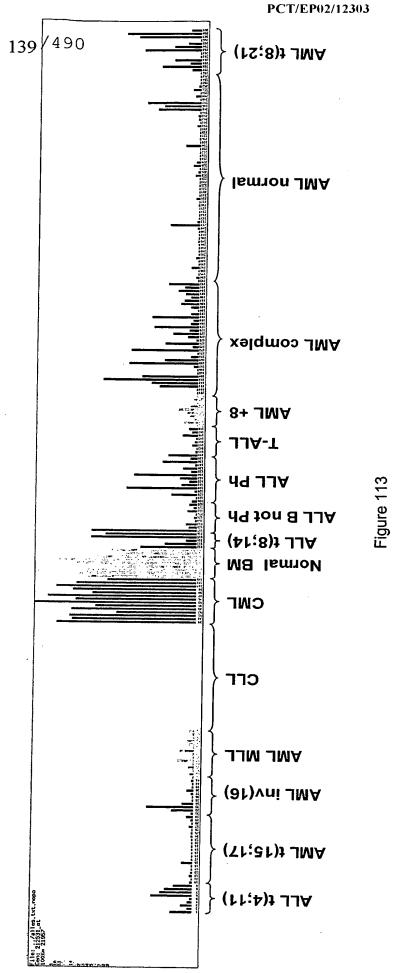
212531\_at, LCN2, CML vs. AML +8



212531\_at, LCN2, CML vs. AML complex



212531\_at, LCN2, CML vs. AML normal

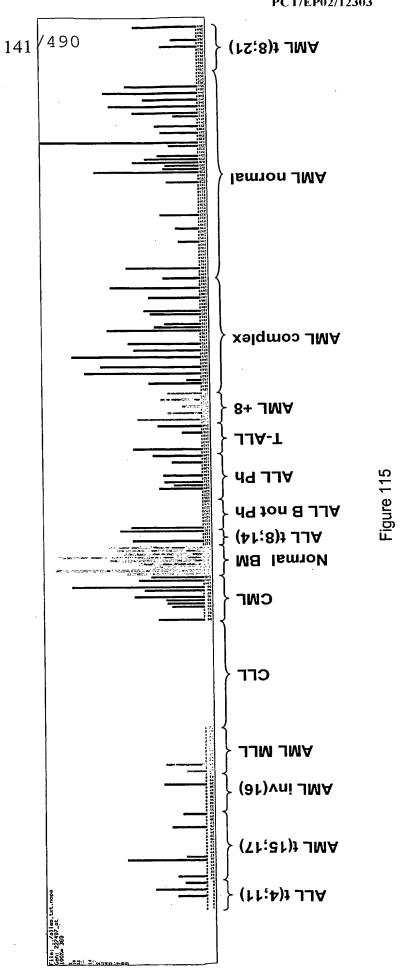


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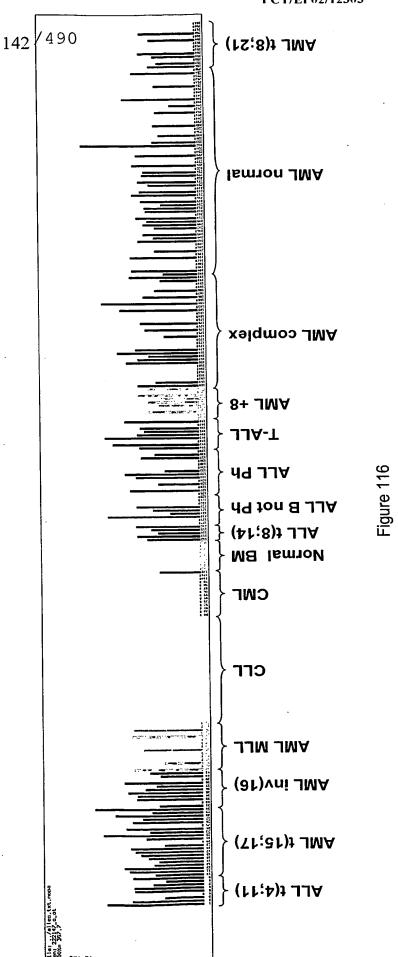


Figure 114

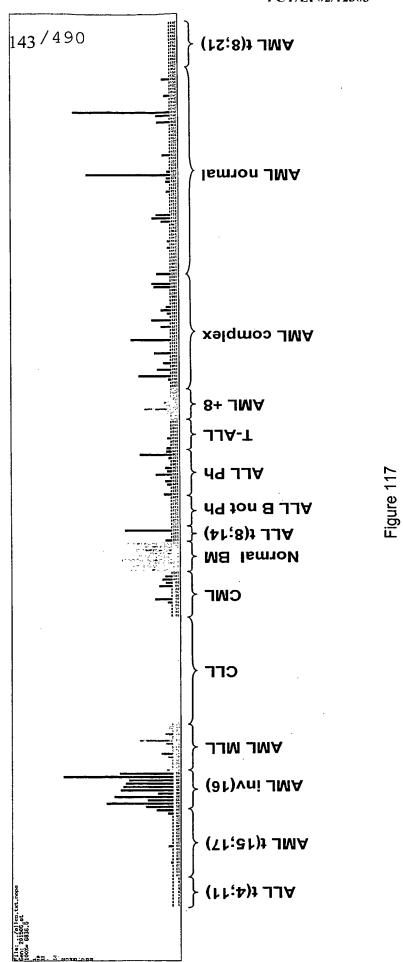
227497\_at, CML vs. all others



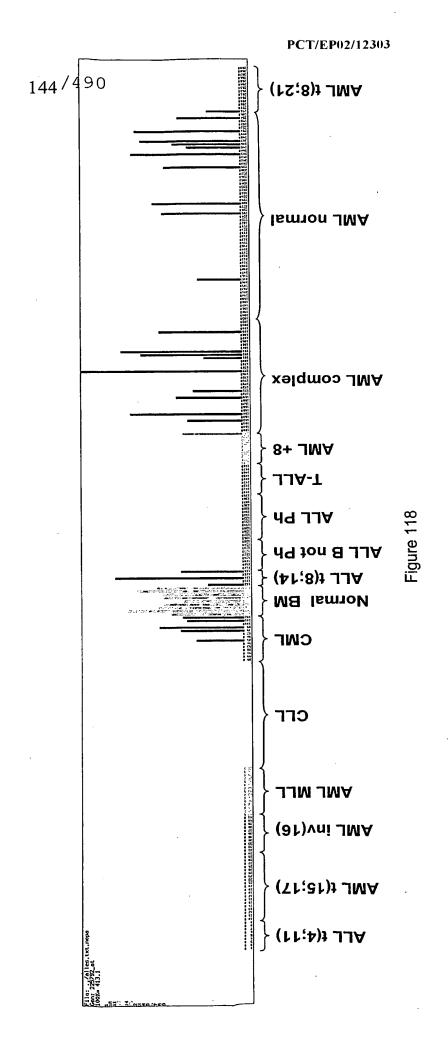
222147\_s\_at, normal BM vs. ALL t(8;14)



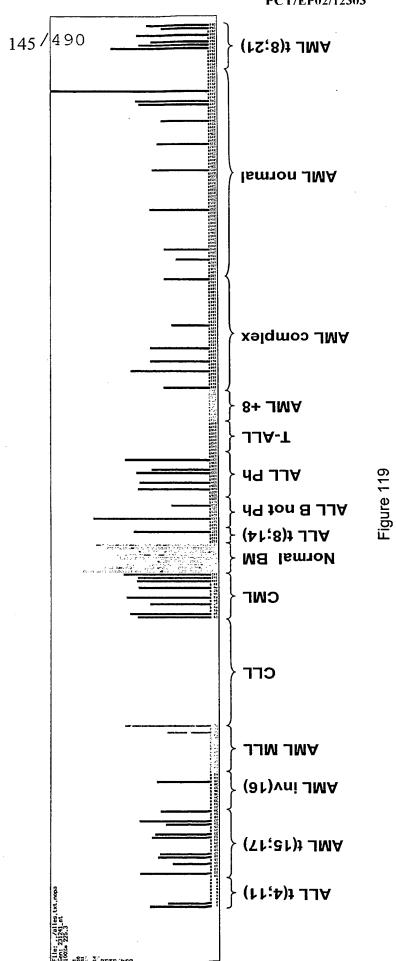
201506\_at, TGFBI, normal BM vs. ALL B not Ph



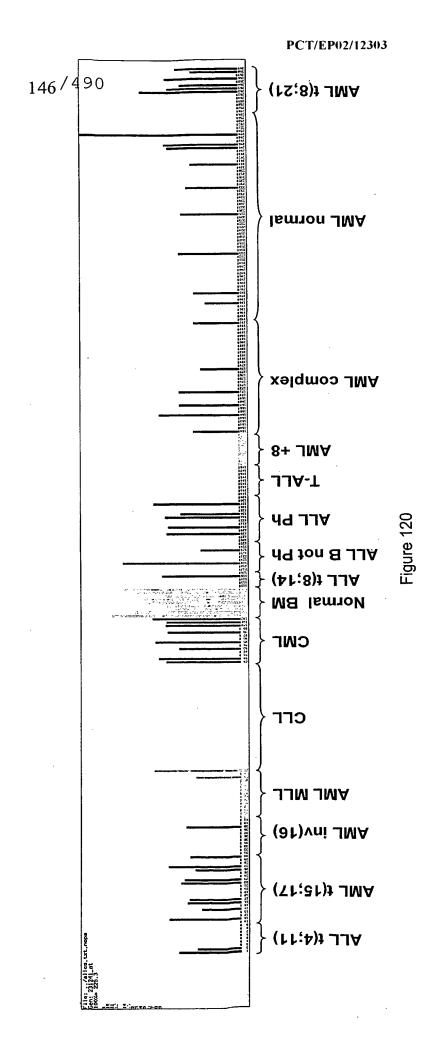




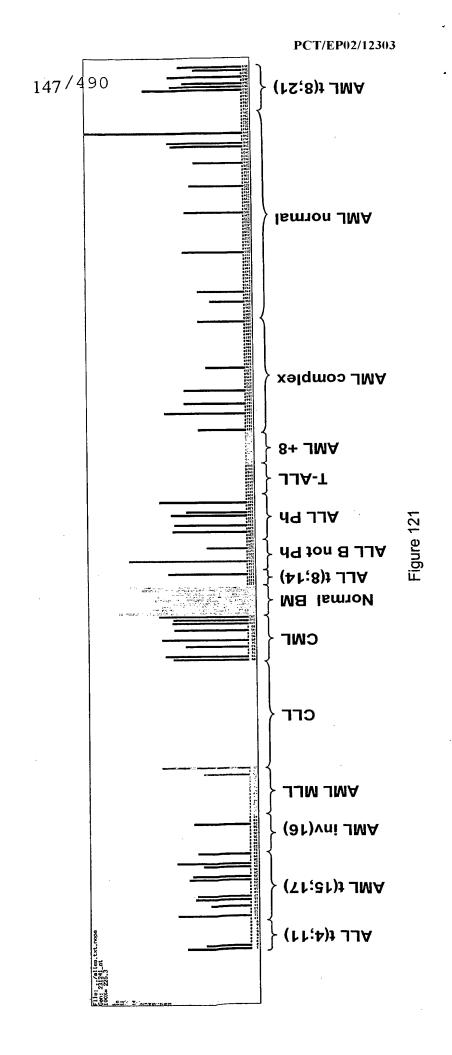
231241\_at, normal BM vs. T-ALL



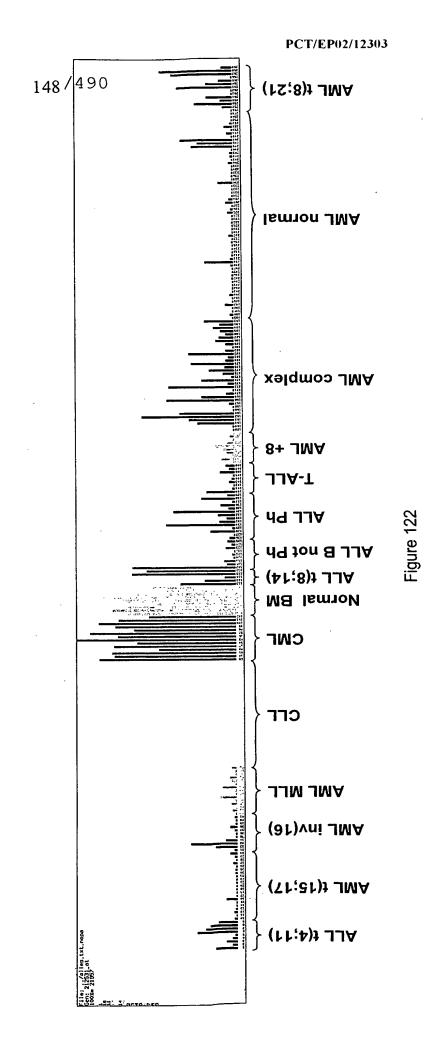
231241\_at, normal BM vs. AML +8

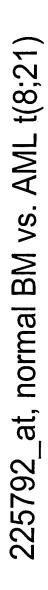


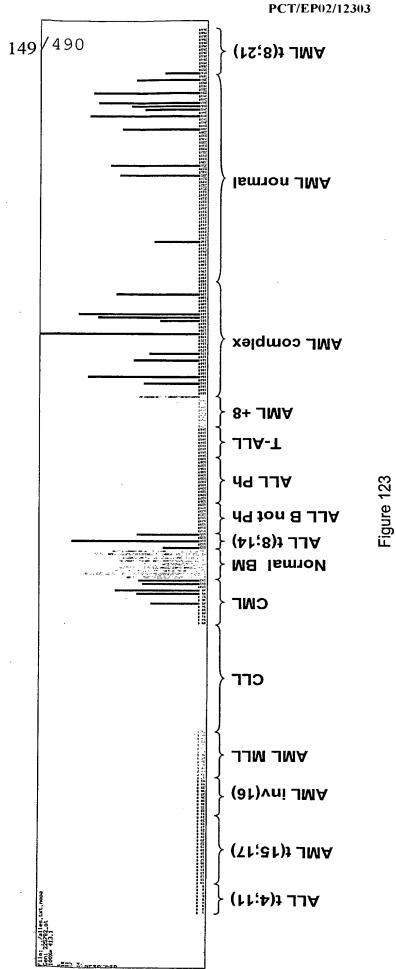
231241\_at, normal BM vs. AML complex



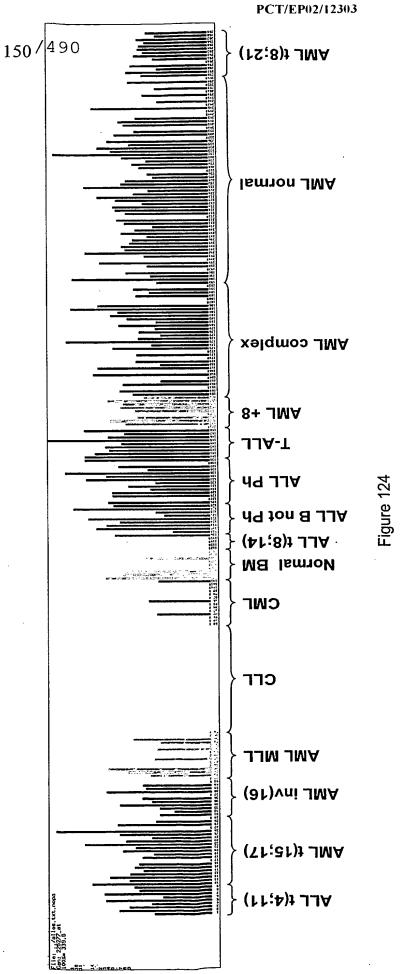
212531\_at, LCN2, normal BM vs. AML normal



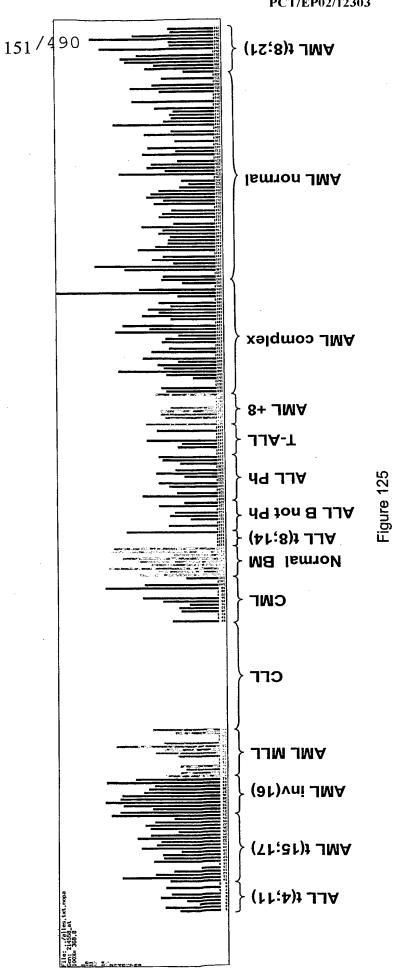




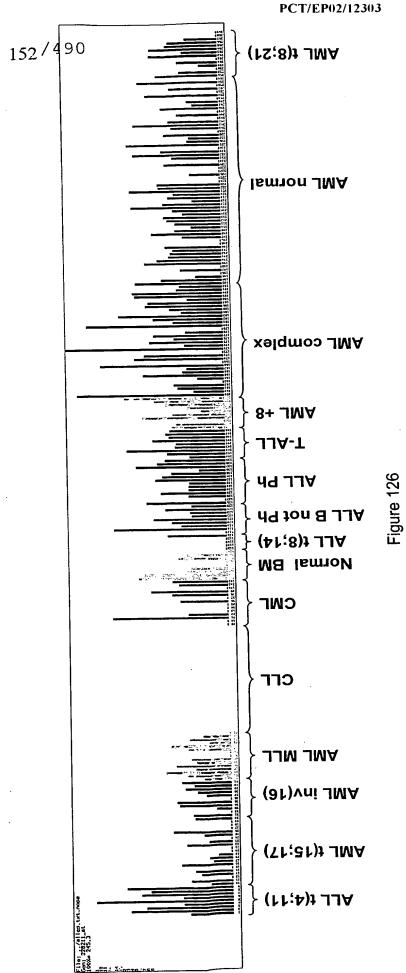
225277\_at, ALL t(8;14) vs. all others



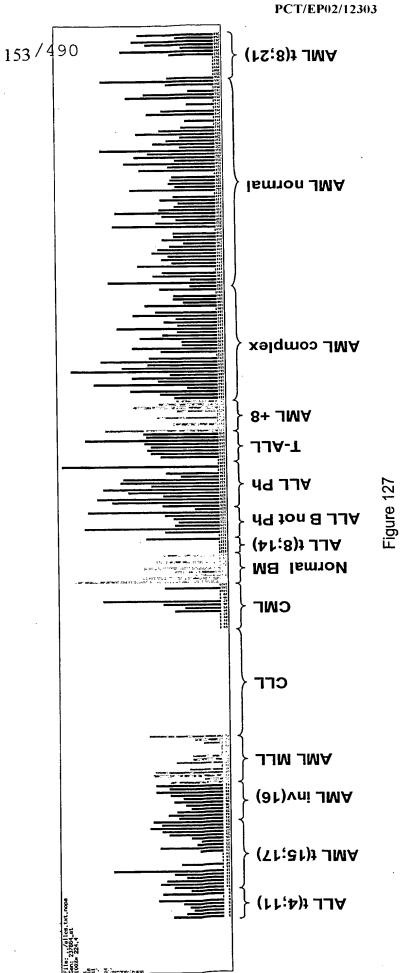




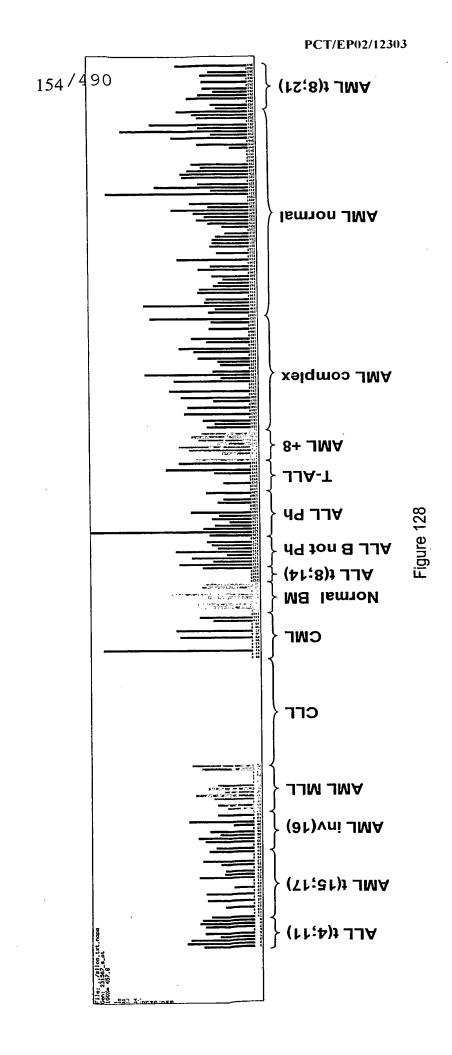




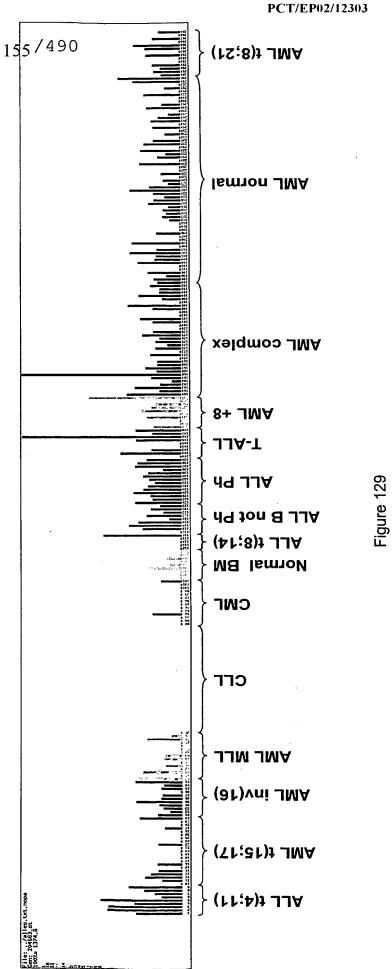
237864\_at, ALL t(8;14) vs. all others



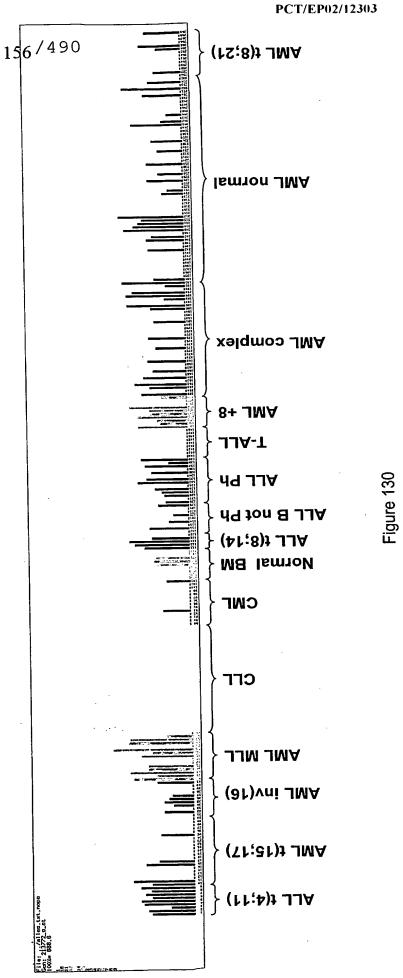




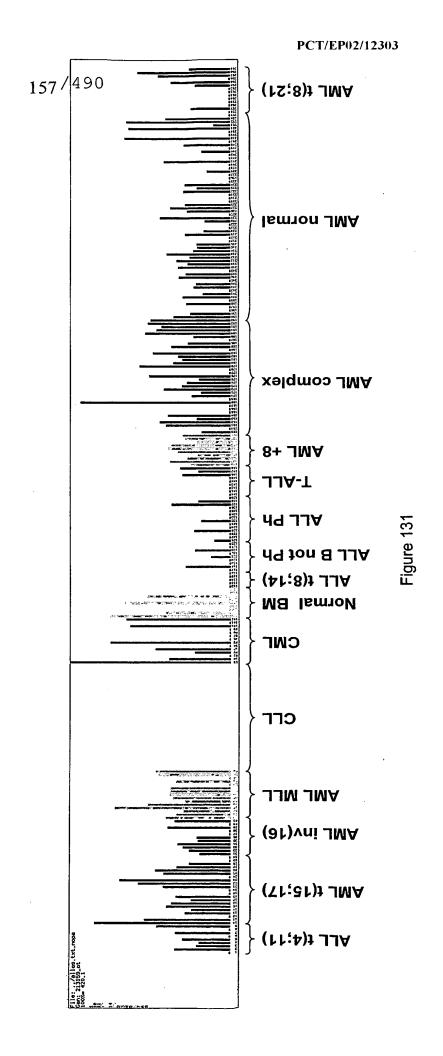
204663\_at, ME3, ALL t(8;14) vs. ALL Ph



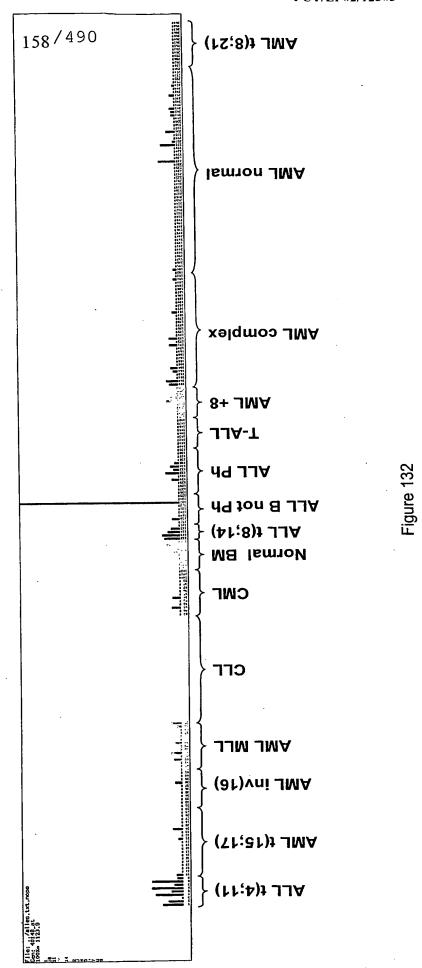




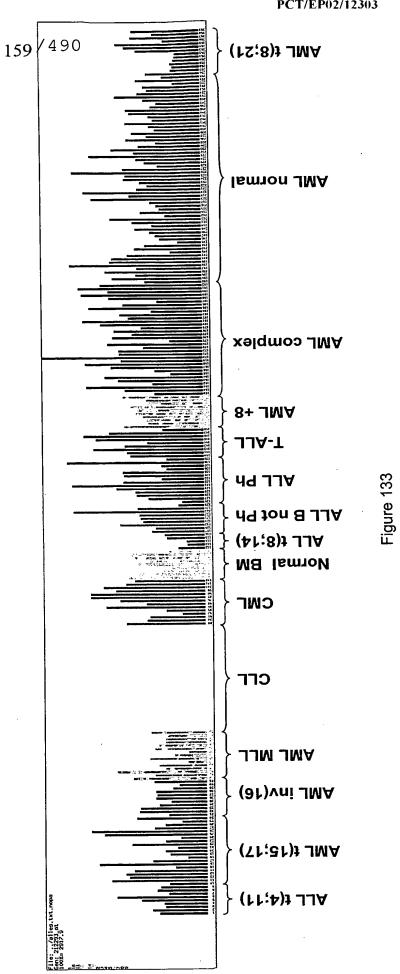
213159\_at, KIAA0805, ALL t(8;14) vs. AML +8



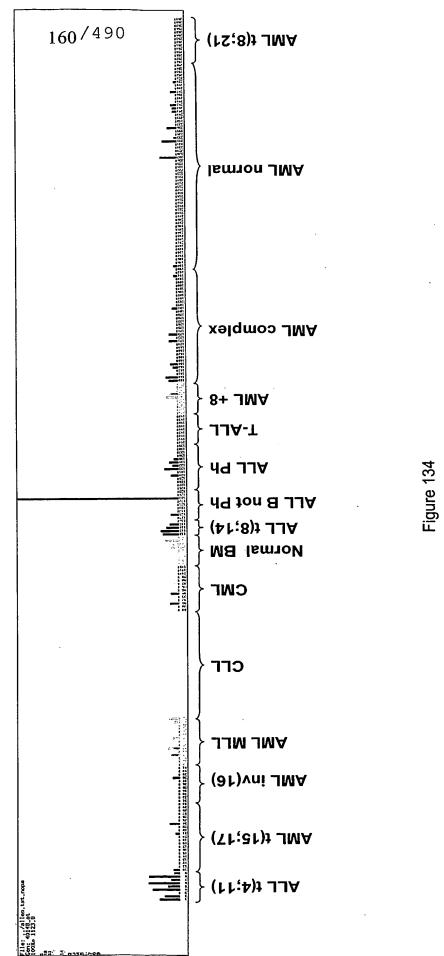




212293\_at, KIAA0630, ALL t(8;14) vs. AML complex

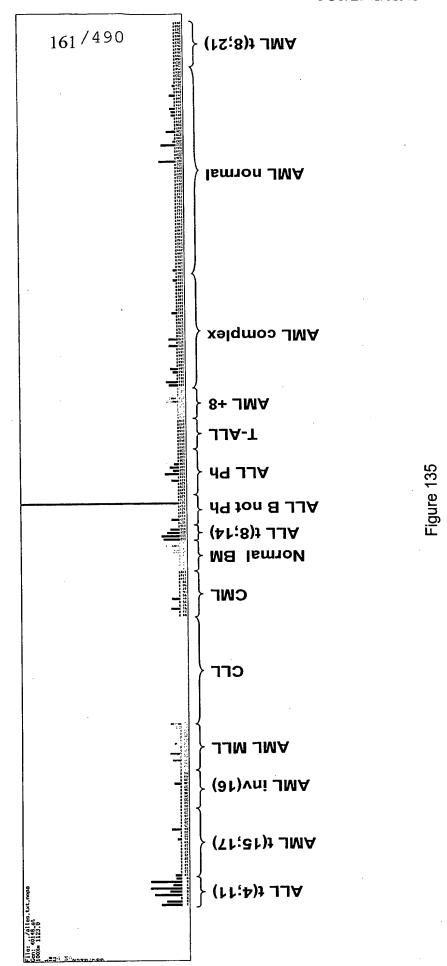


40148\_at, APBB2, ALL t(8;14) vs. AML normal

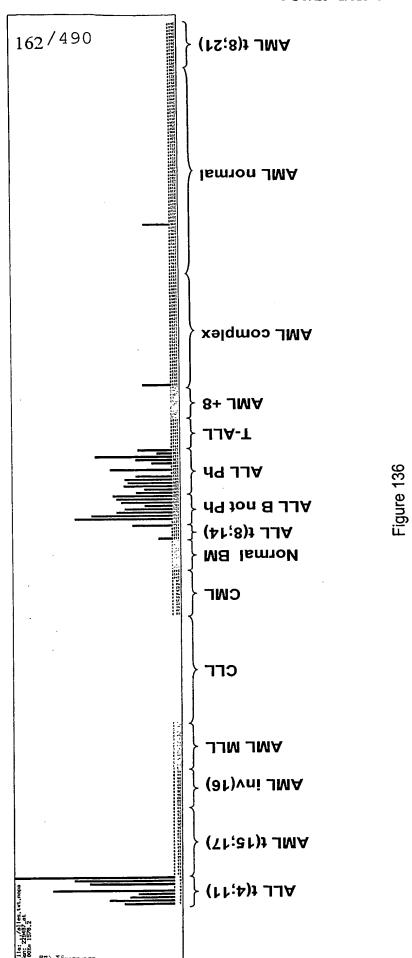


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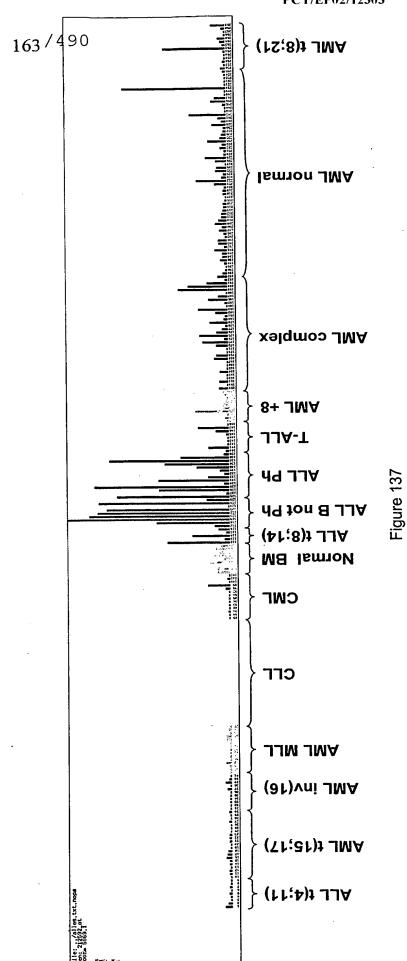
\_\_\_03039443**A**2\_l\_>



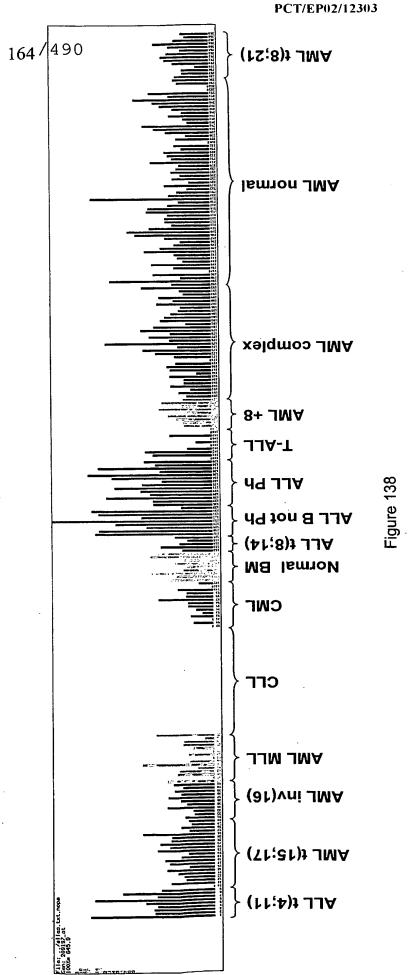
## 229487\_at, ALL B nicht Ph vs. all others



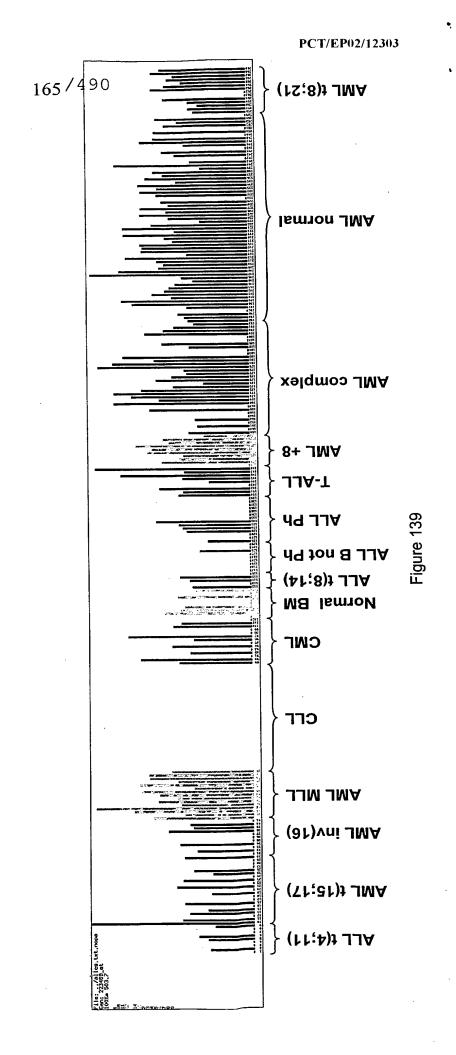




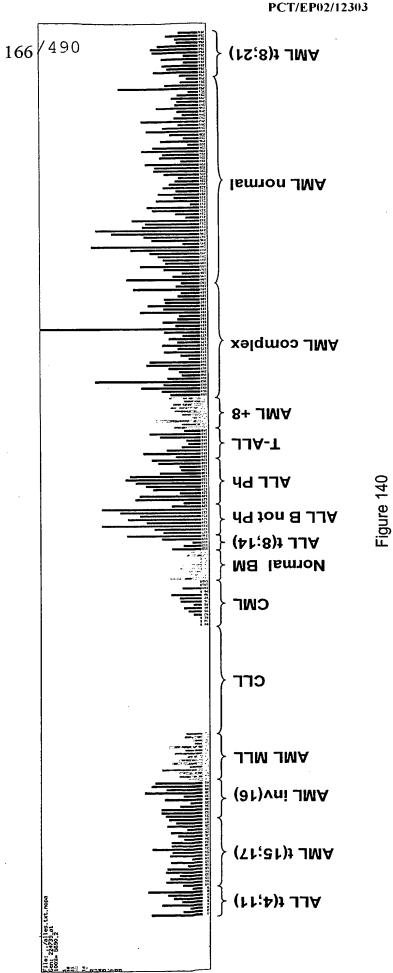




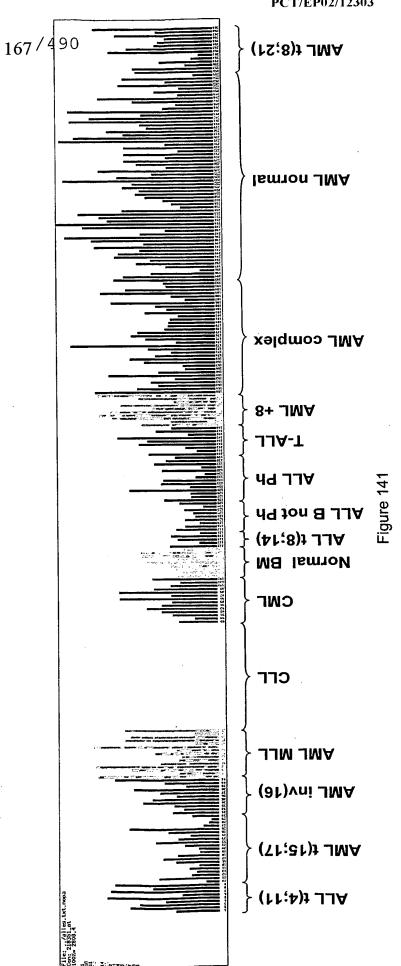




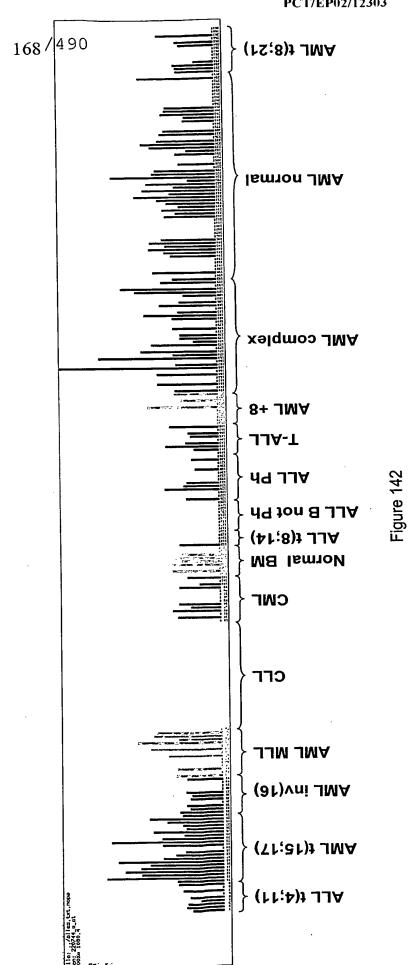
224739\_at, MG61, ALL B not Ph vs. all others



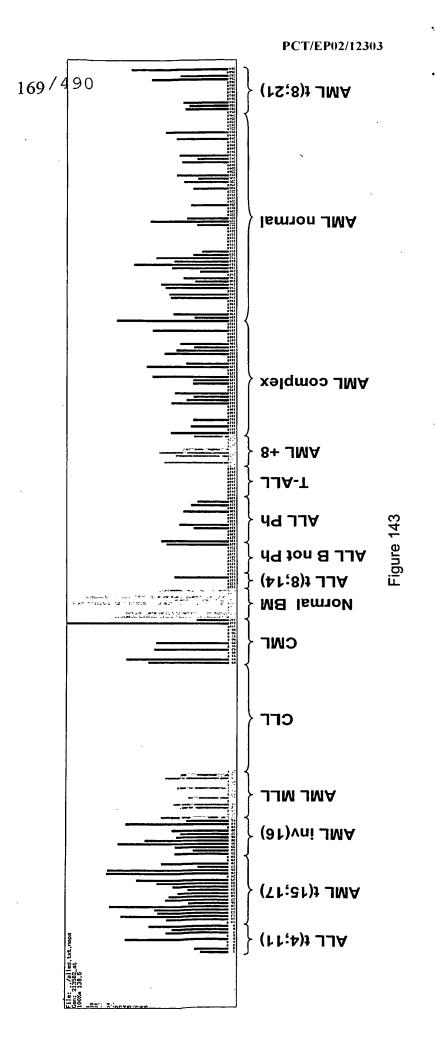




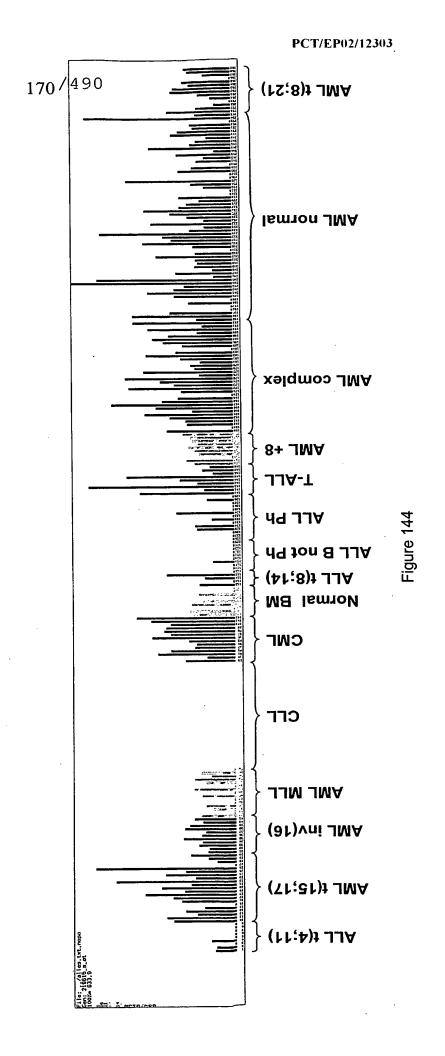
220744\_s\_at, WDR10, ALL B not Ph vs. all others



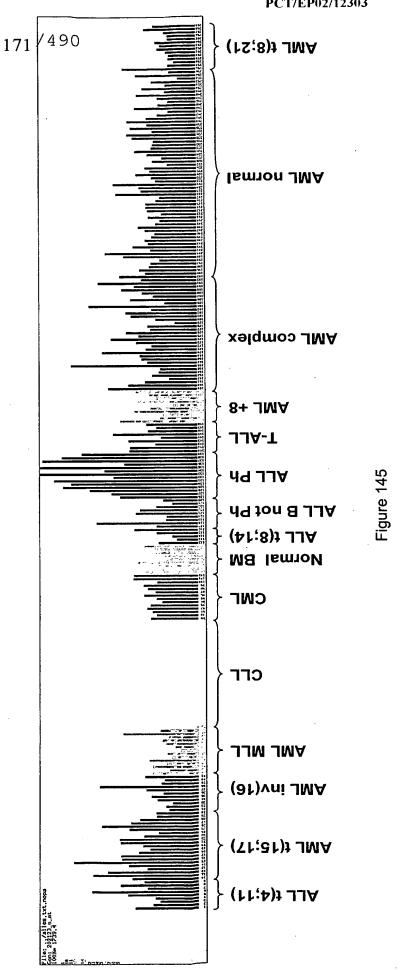
213582\_at, ATP11A, ALL B not Ph vs. all others



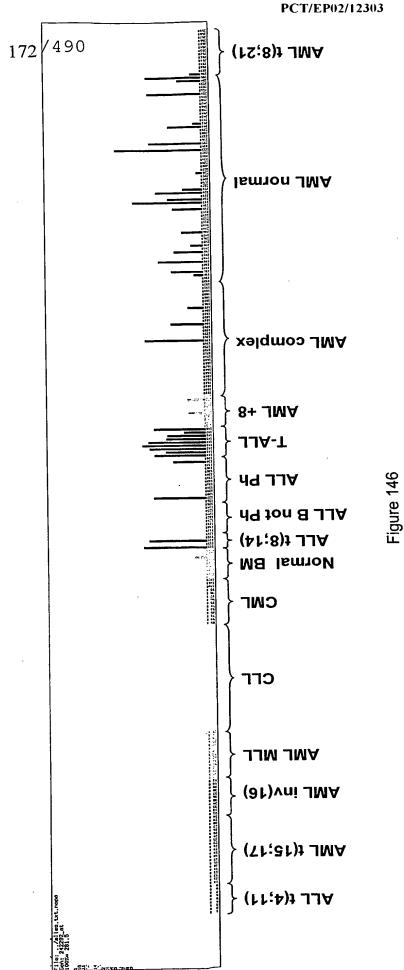
219615\_s\_at, KCNK5, ALL B not Ph vs. all others



202123\_s\_at, ABL1, ALL B not Ph vs. ALL Ph

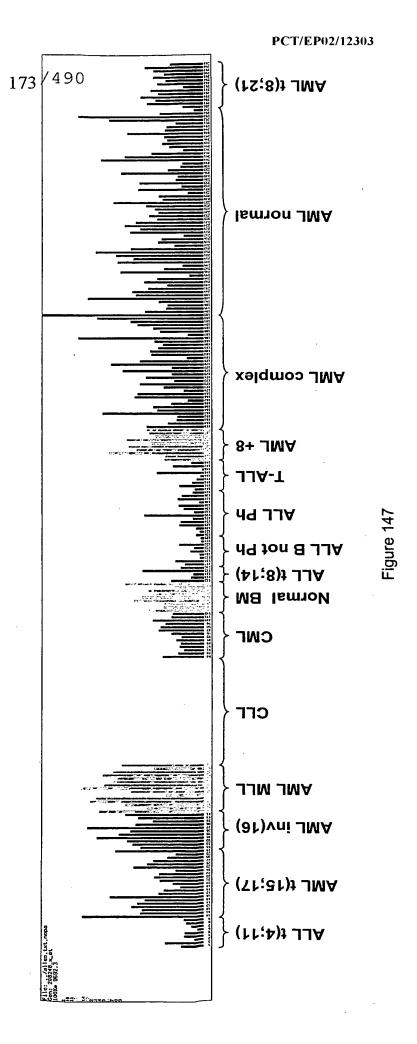




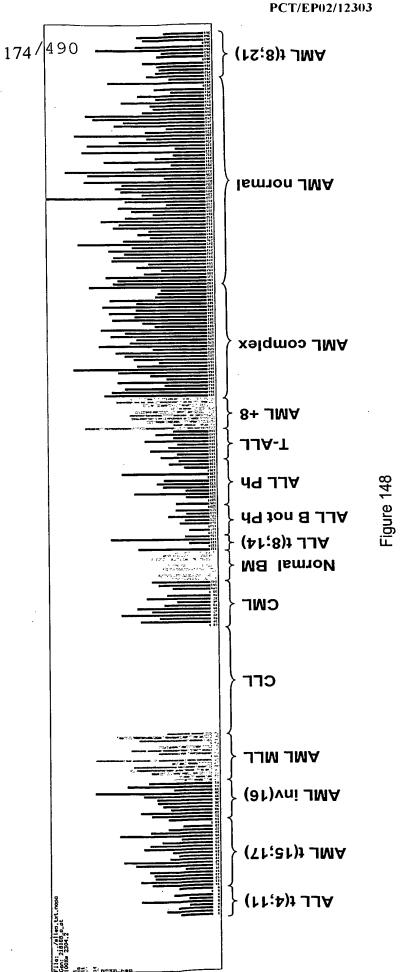


\_\_\_\_03039443A2\_i\_> BNSDOCID: <WO\_

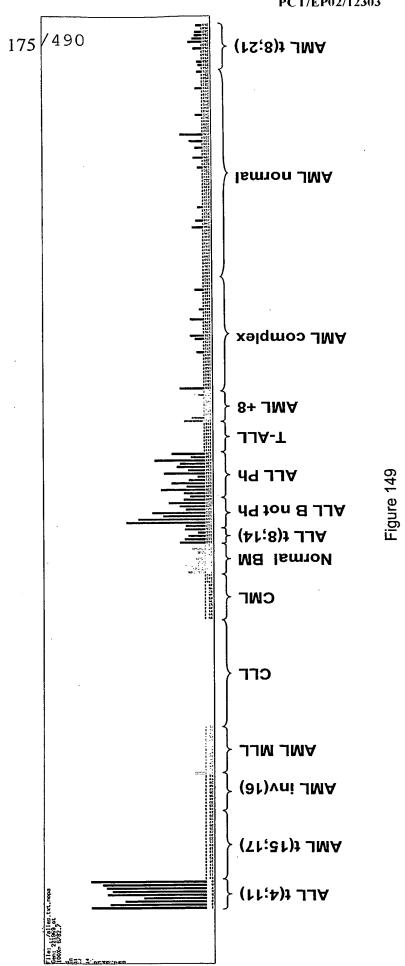
WO 03/039443



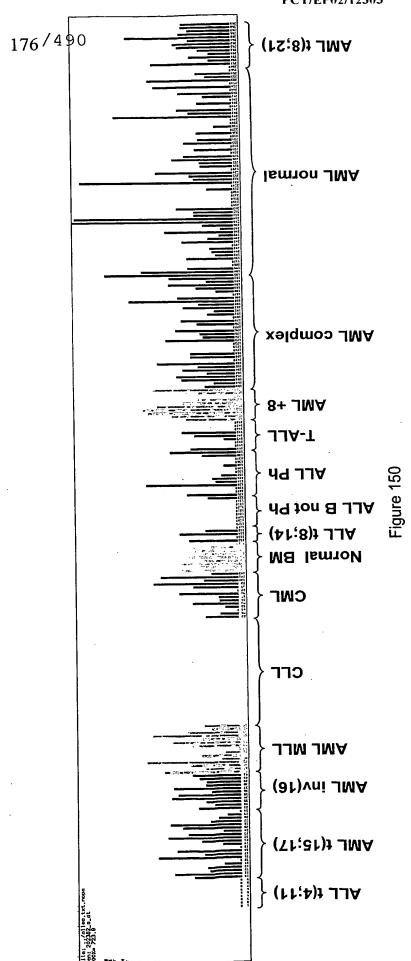
218168\_s\_at, CABC1, ALL B not Ph vs. AML complex



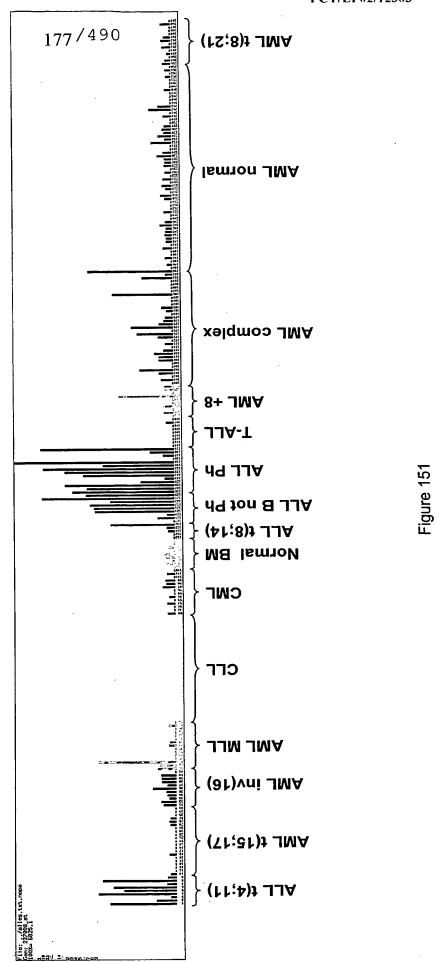




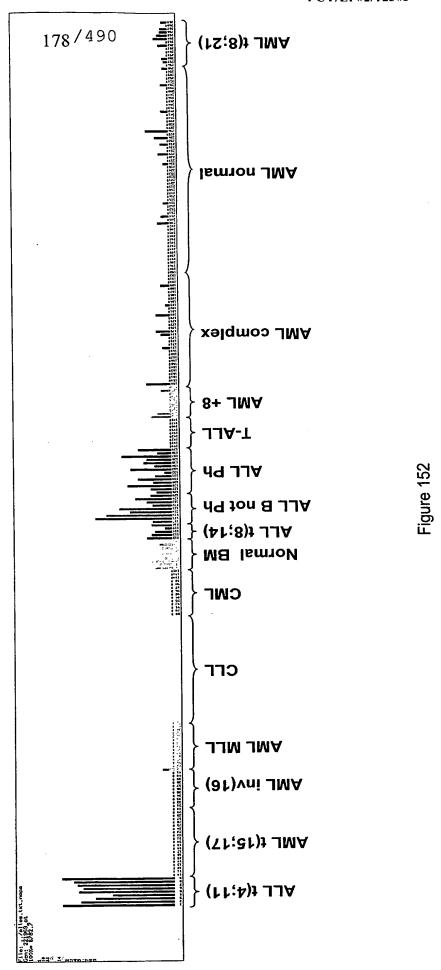




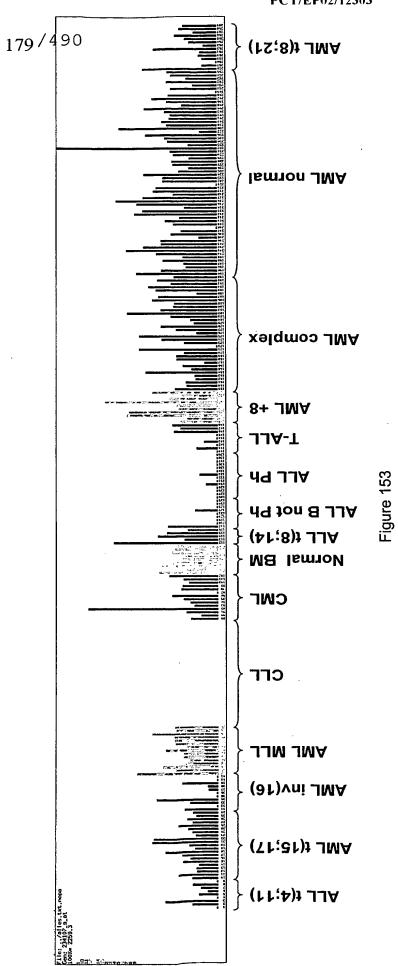
227998\_at, MGC17528, ALL Ph vs. all others



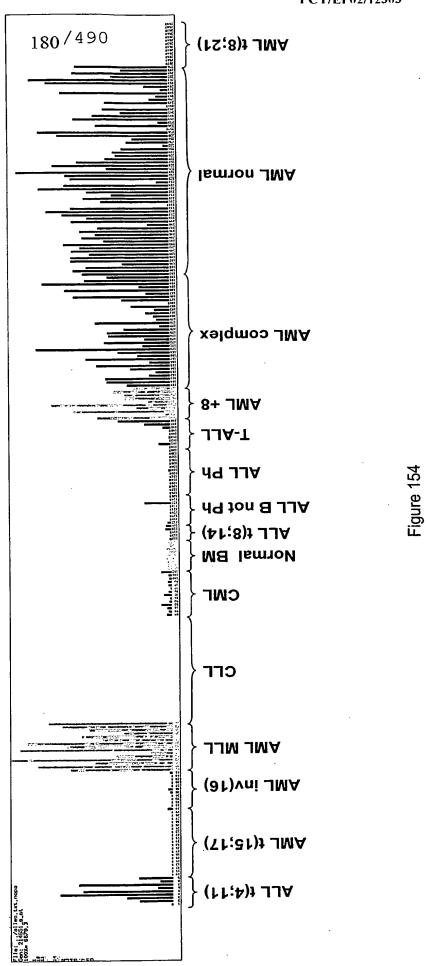
221969\_at, PAX5, ALL Ph vs. T-ALL



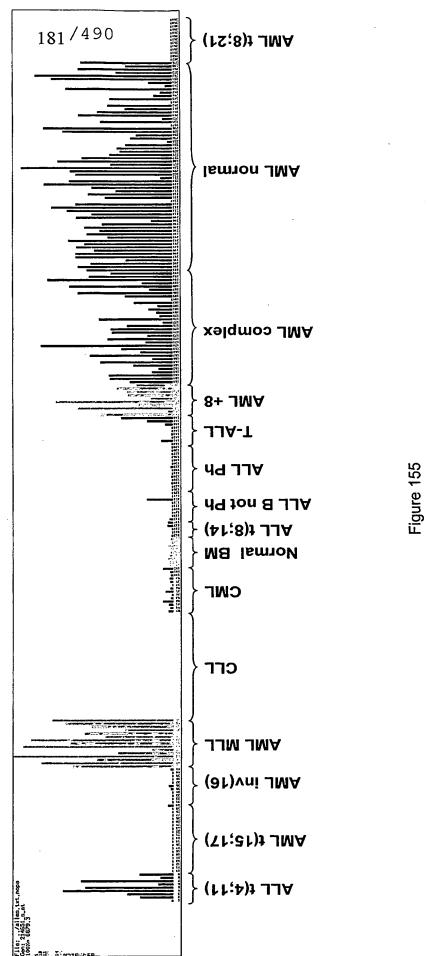
234107\_s\_at, ALL Ph vs. AML +8



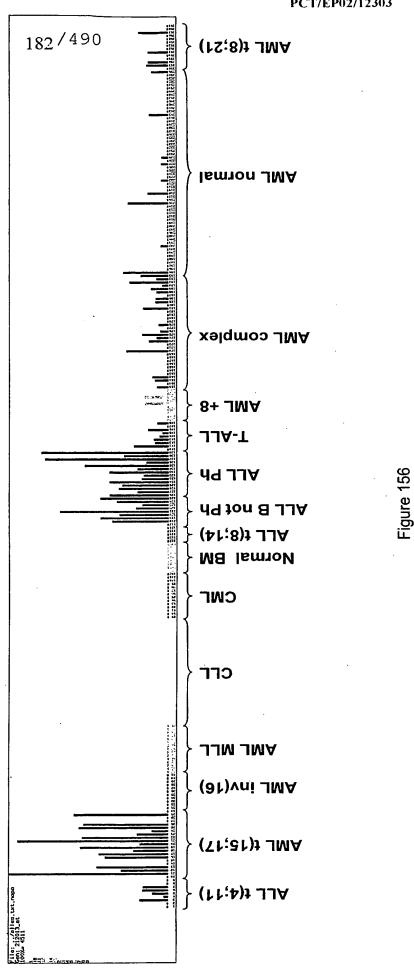
## 214641\_s\_at, HOXA9, ALL Ph vs. AML complex



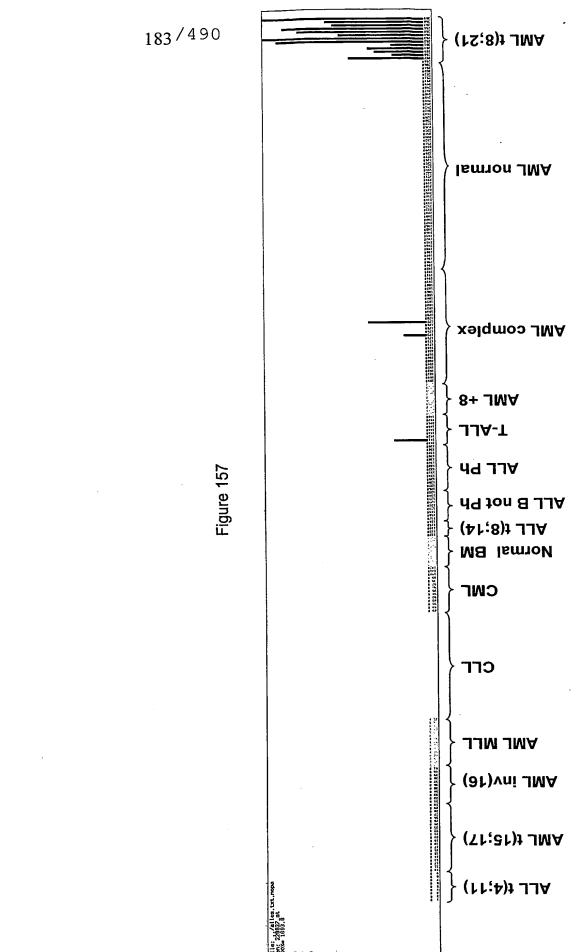
## 214641\_s\_at, HOXA9, ALL Ph vs. AML normal



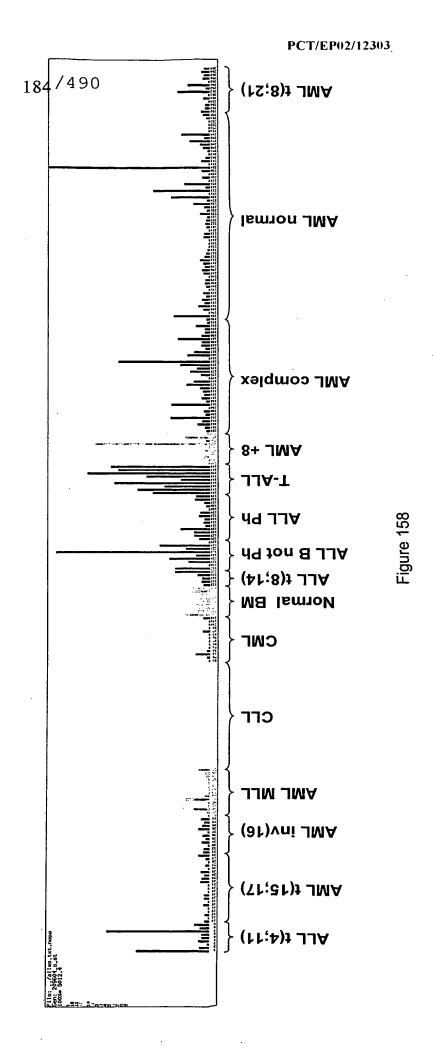
## 212013\_at, D2S448, ALL Ph vs. AML normal



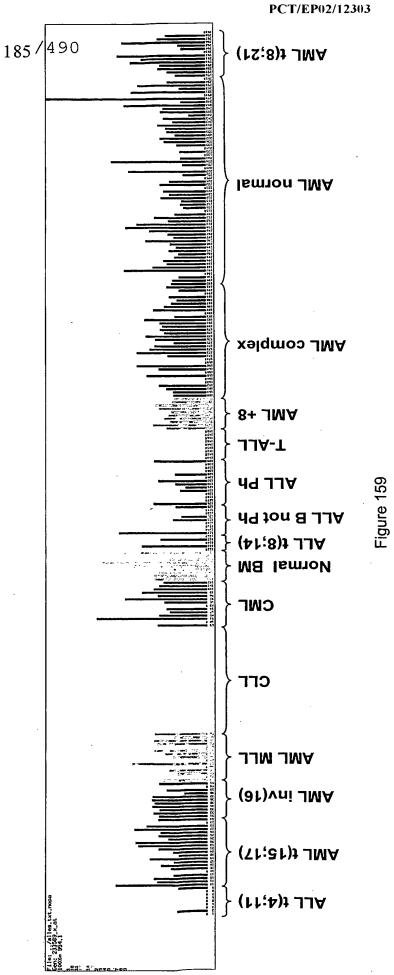
228827\_at, ALL Ph vs. AML t(8;21)



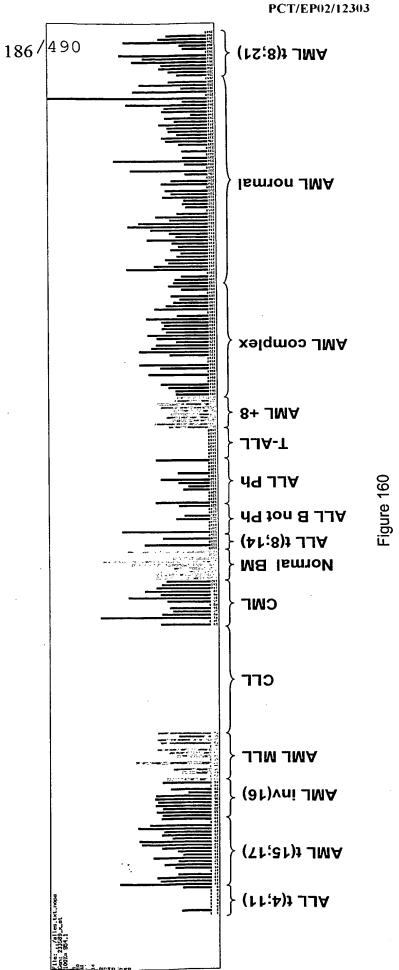
209604\_s\_at, GATA3, T-ALL vs. all others



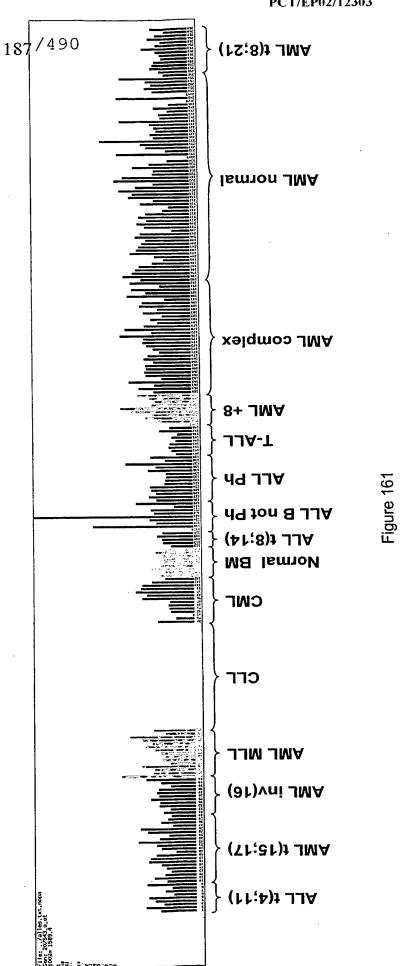
233589\_x\_at, T-ALL vs. all others



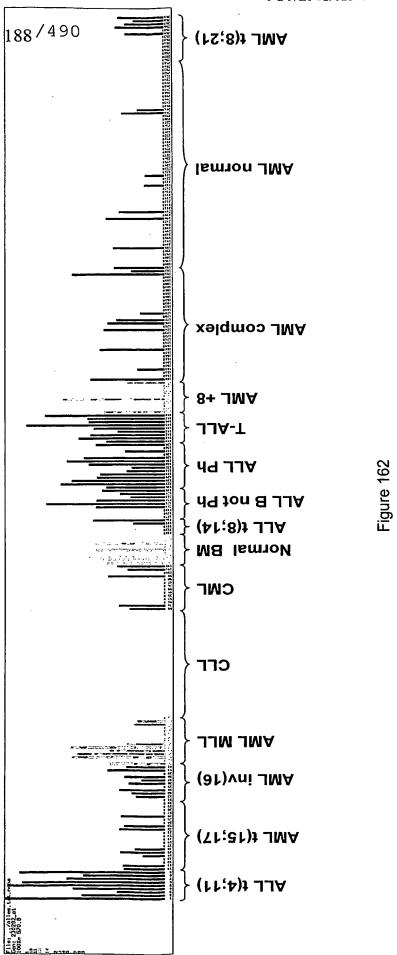
233589\_x\_at, T-ALL vs. AML +8



207543\_s\_at, P4HA1, T-ALL vs. AML complex







(rr;4)1 JJA

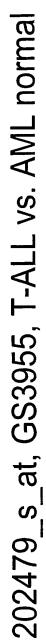
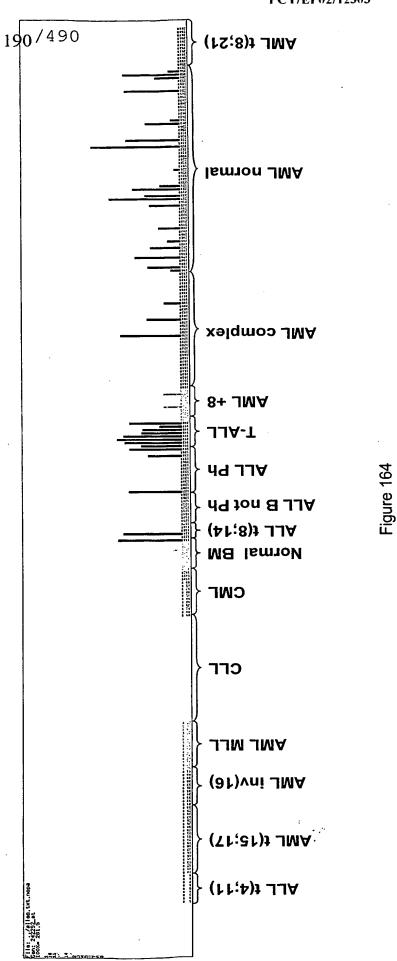
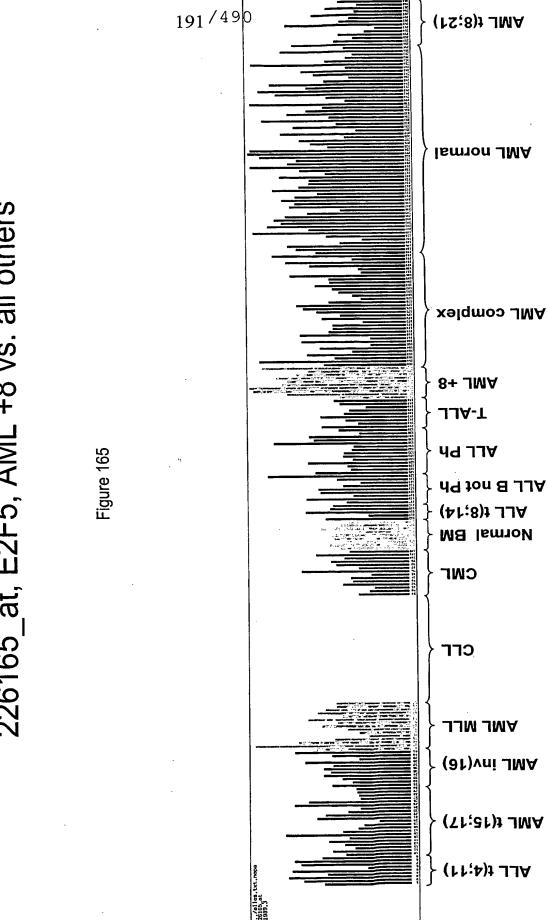


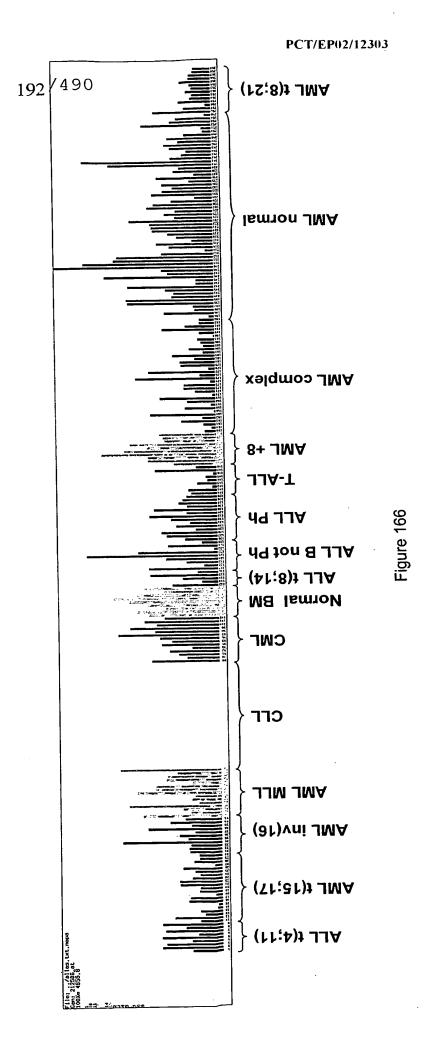
Figure 163



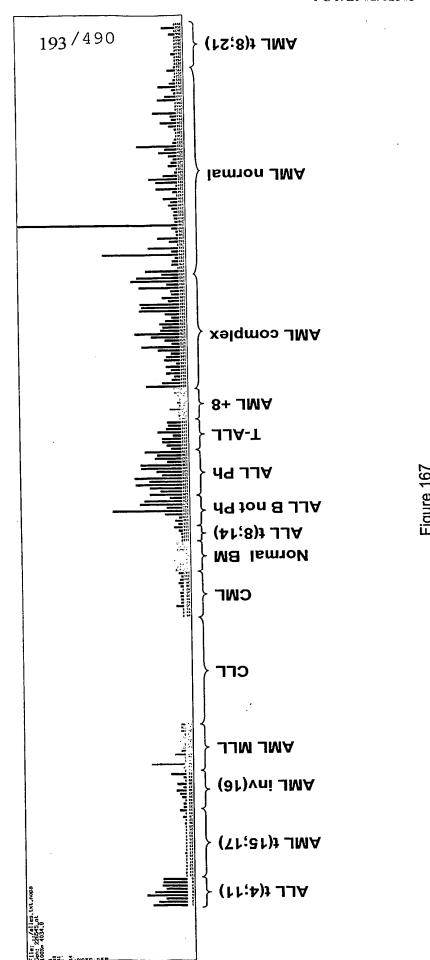


## 226165\_at, E2F5, AML +8 vs. all others

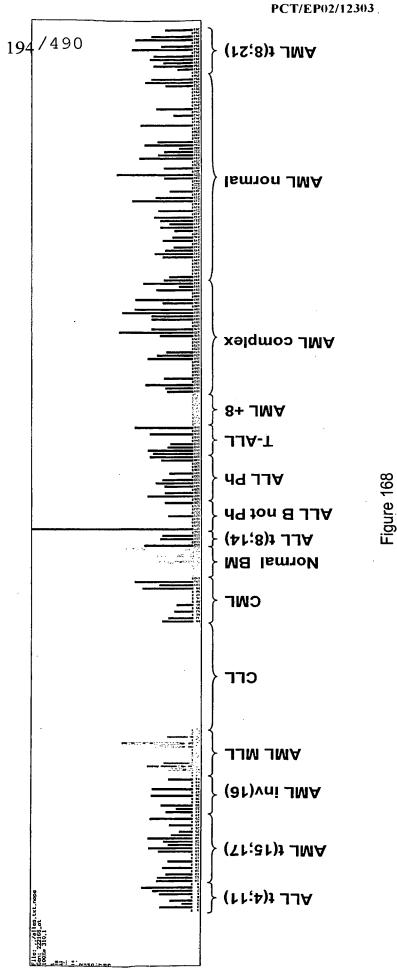




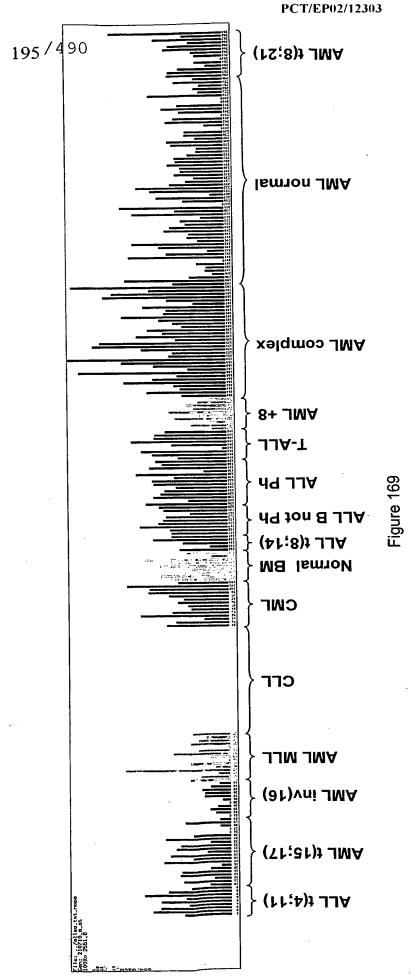
226545\_at, AML +8 vs. AML complex



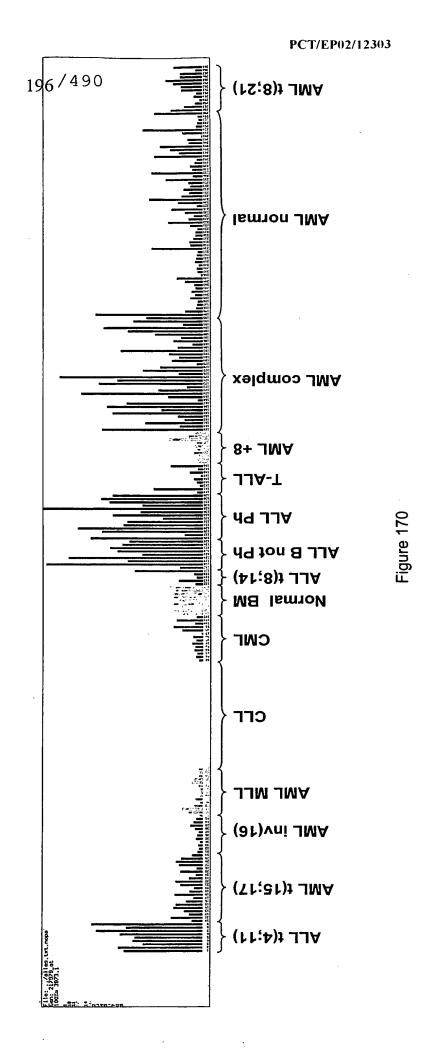
222166\_at, AML +8 vs. AML complex



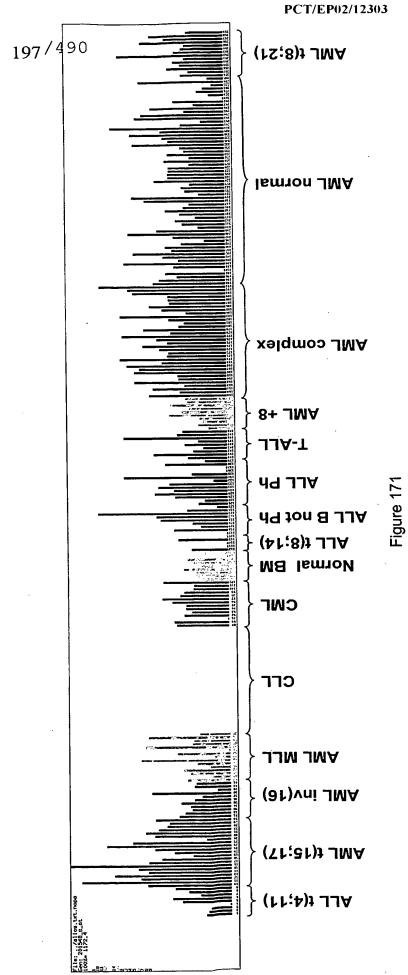
210715\_s\_at, SPINT2, AML +8 vs. AML complex



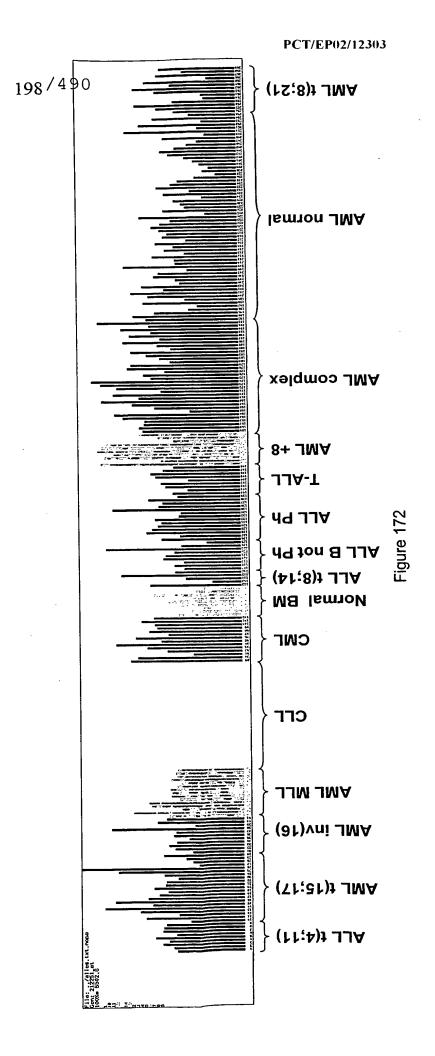
217979\_at, NET-6, AML +8 vs. AML complex



201548\_s\_at, PLU-1, AML +8 vs. AML complex

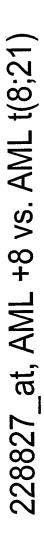


212251\_at, AML +8 vs. AML normal

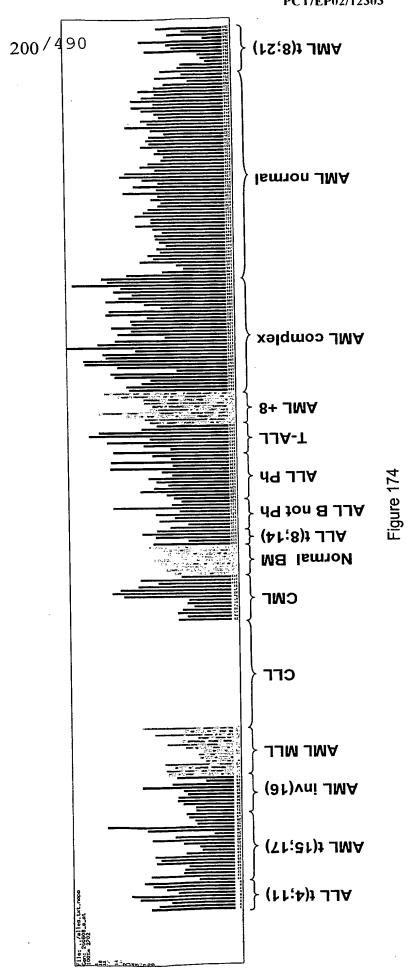


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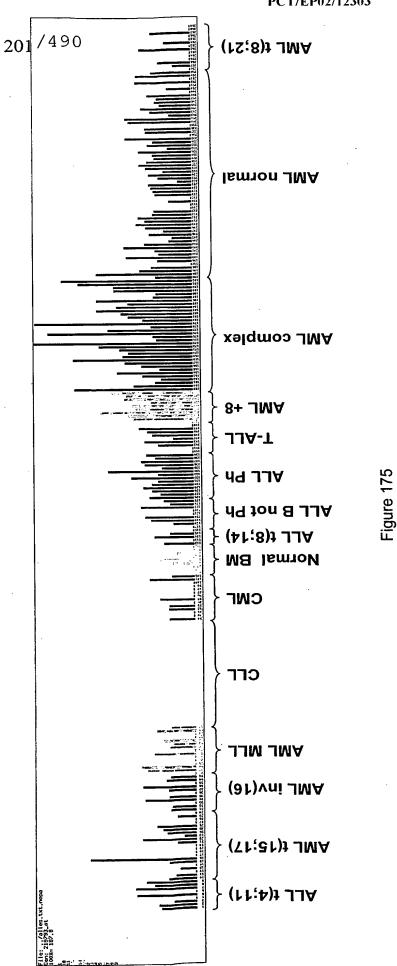
PCT/EP02/12303



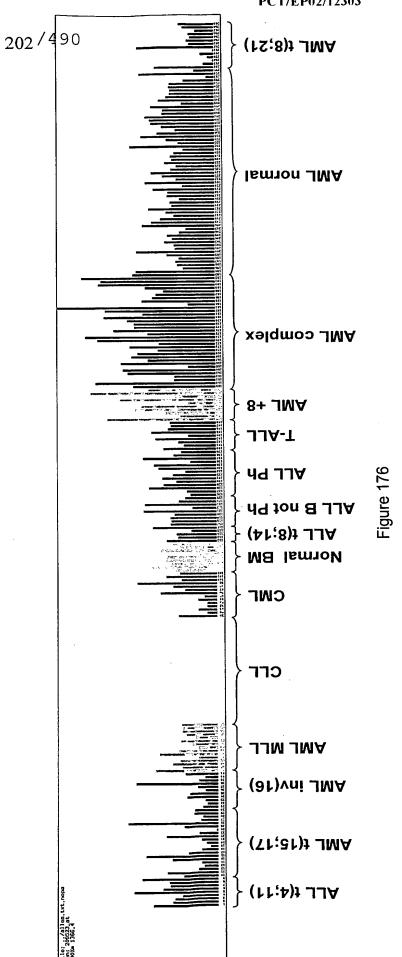




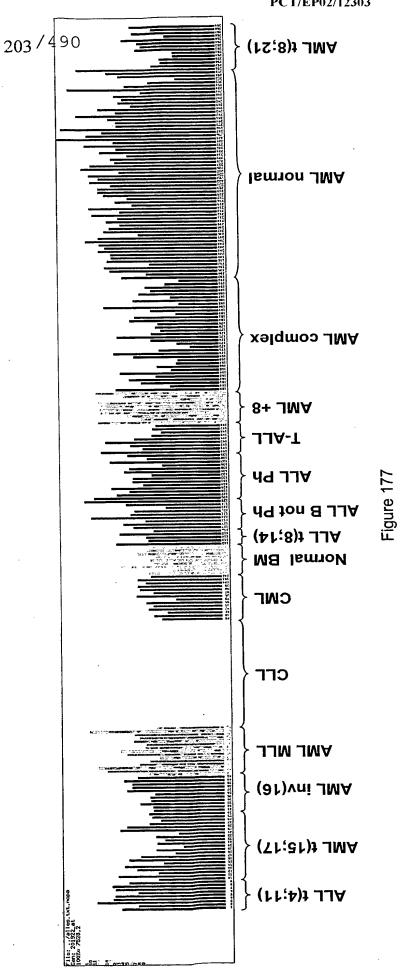
219793\_at, SNX16, AML complex vs. all others

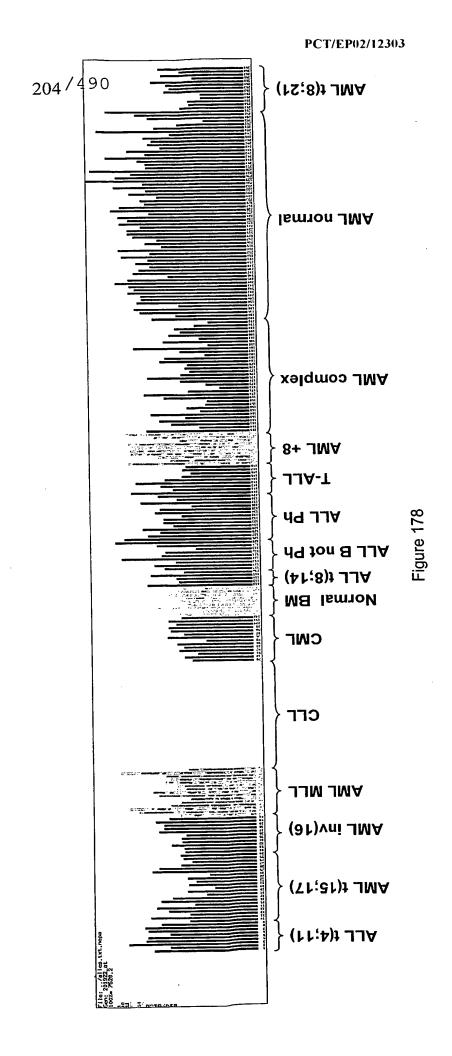


209523\_at, AML complex vs. all others

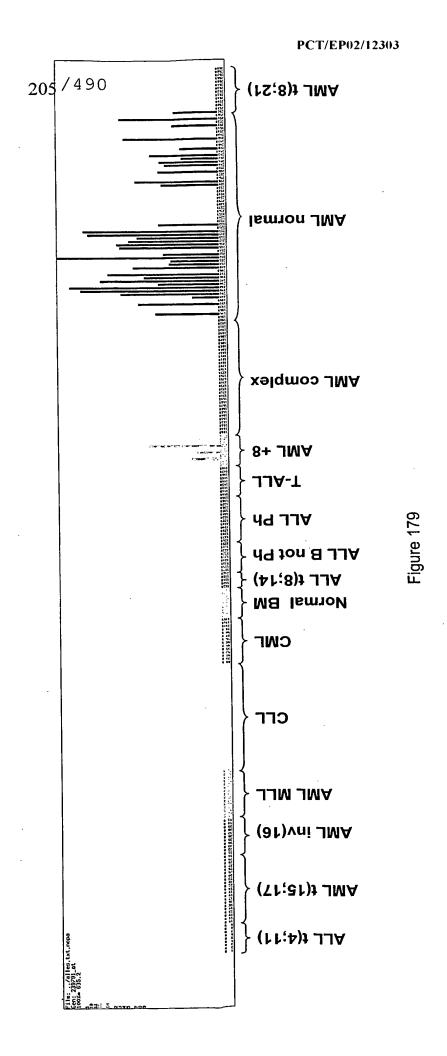


200093\_s\_at - HG-U133B, HINT1, AML complex vs. AML normal

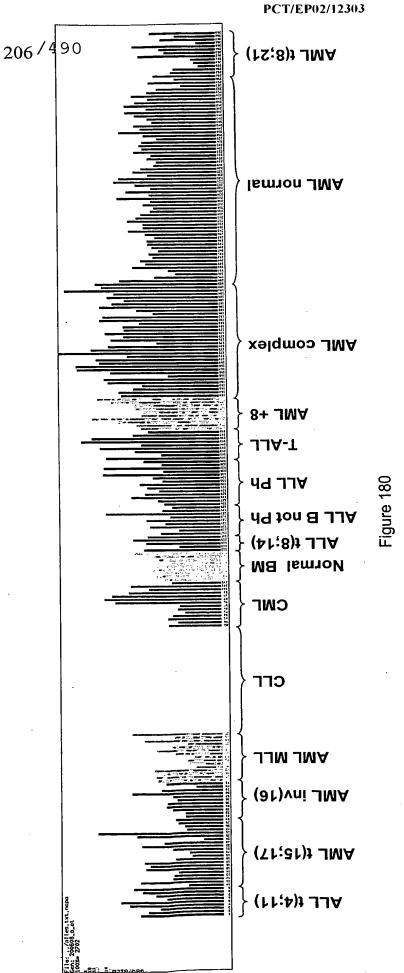




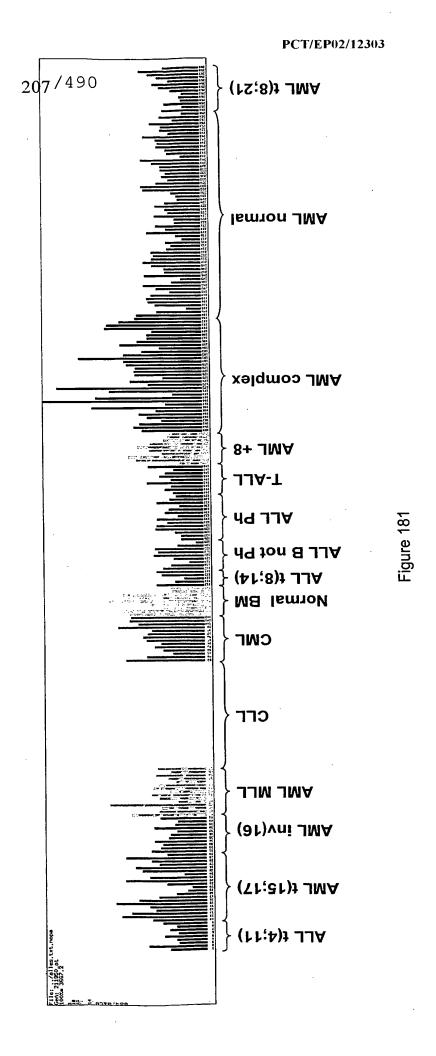
239791\_at, HOXB6, AML complex vs. AML normal



200608\_s\_at, RAD21, AML complex vs. AML normal



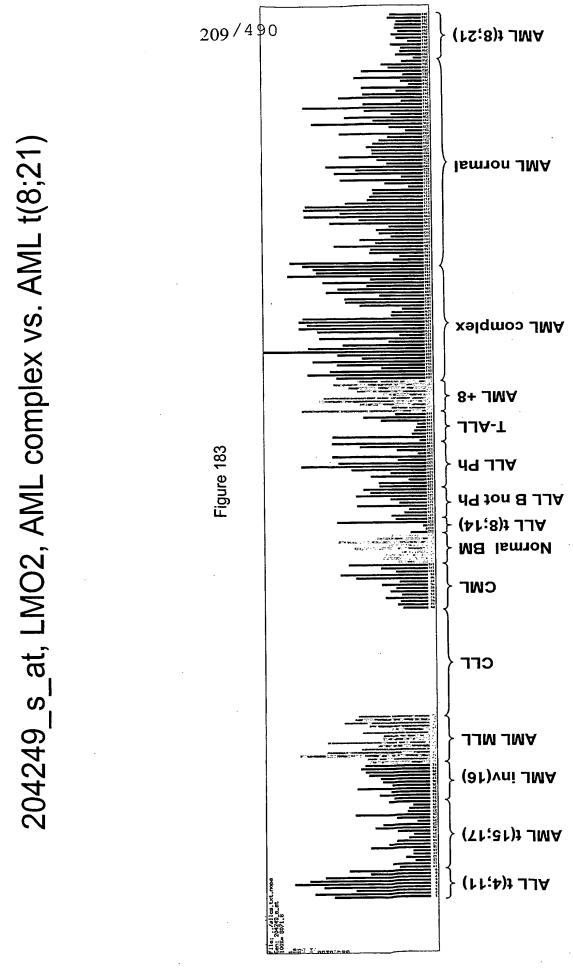
211950\_at, RBAF600, AML complex vs. AML normal



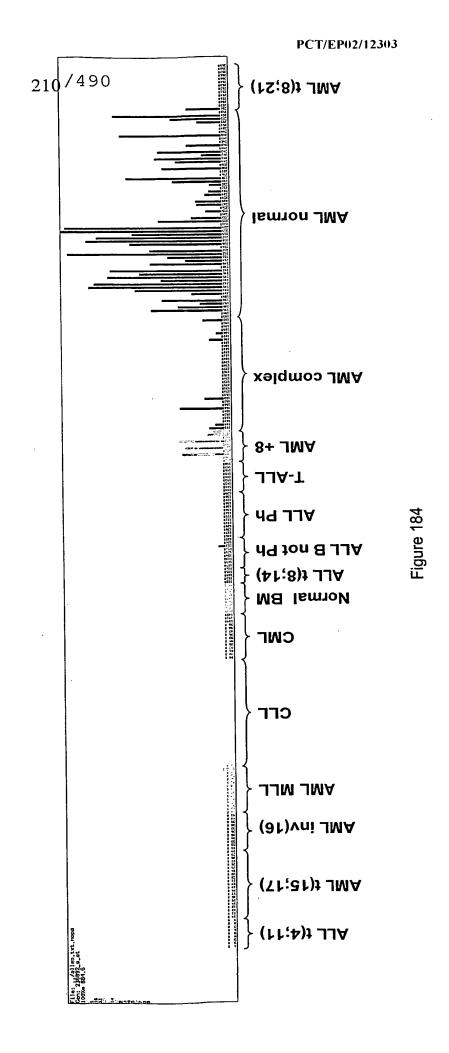
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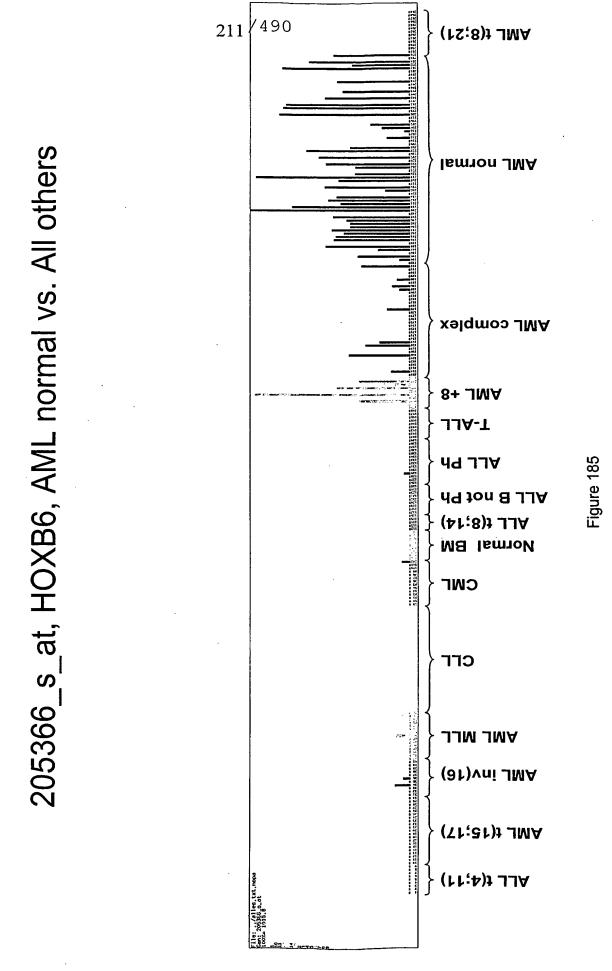
PCT/EP02/12303

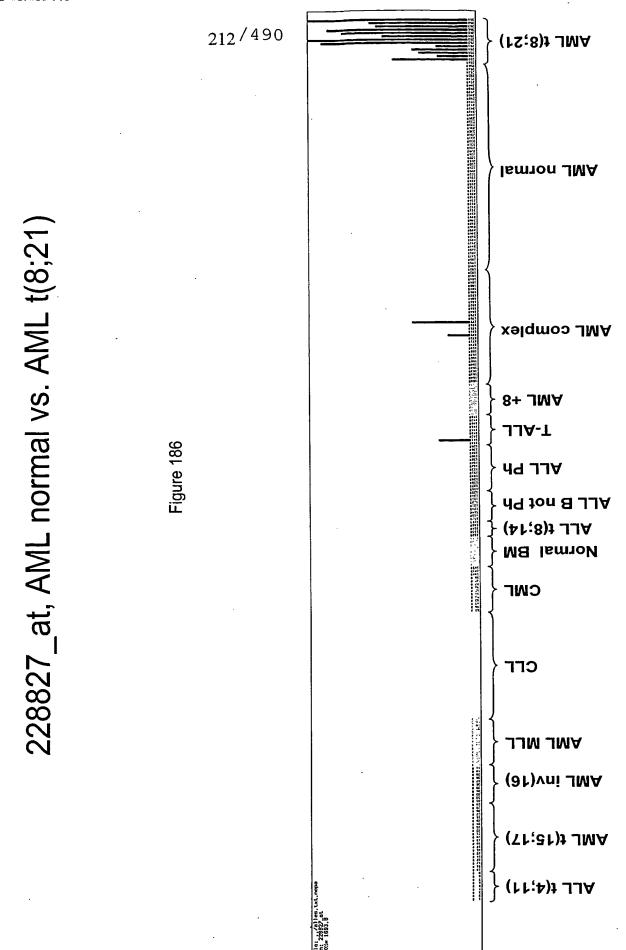




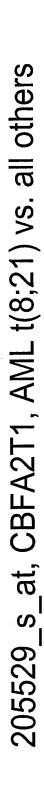
236892\_s\_at, HOXB6, AML normal vs. all others

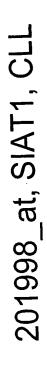


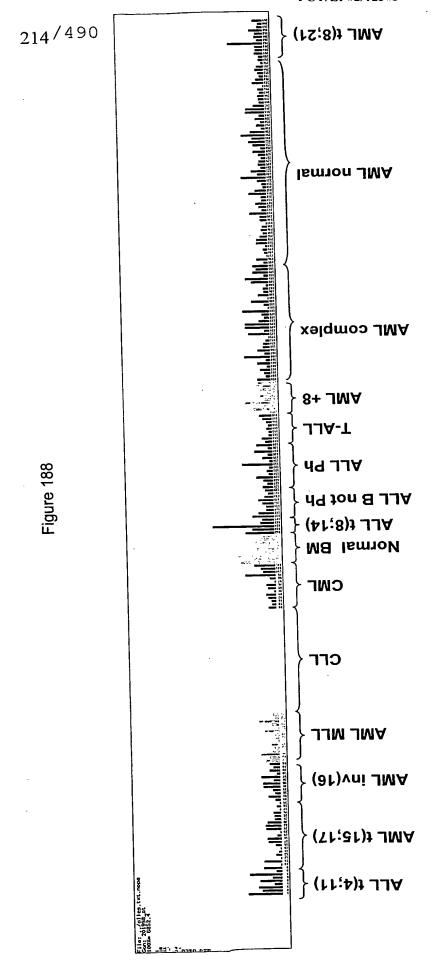




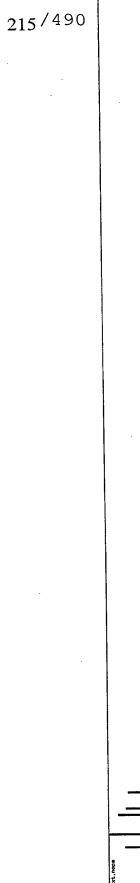
PCT/EP02/12303

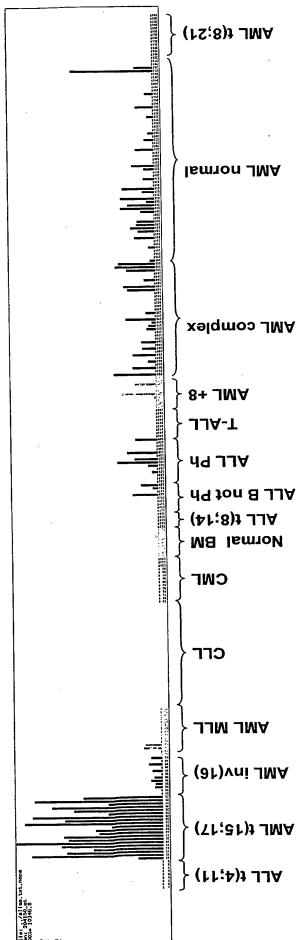






## 204150\_at, STAB1, AML t(15;17)

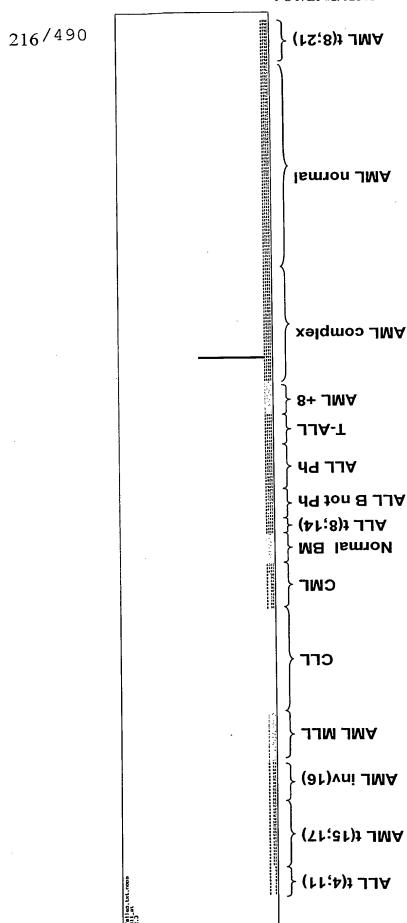


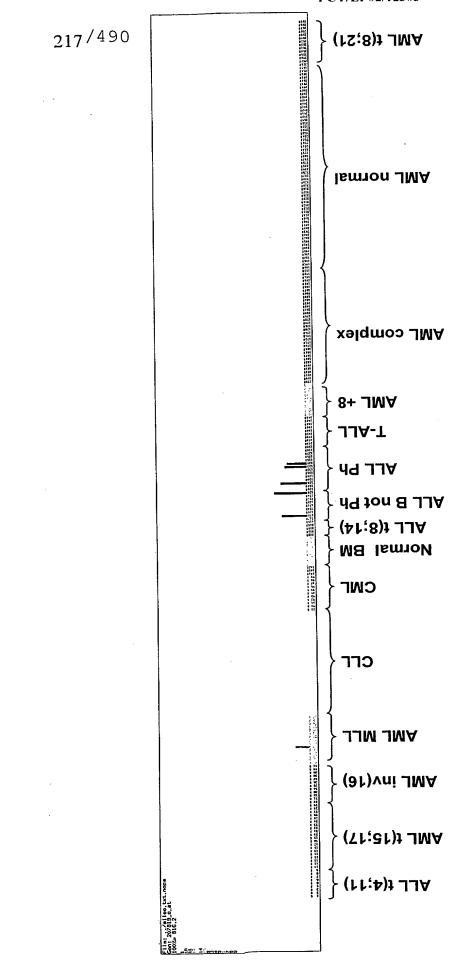




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Figure 190





207819\_s\_at, ABCB4, CLL

205805\_s\_at, ROR1, CLL

Figure 192

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(Tr;81)3 JMA

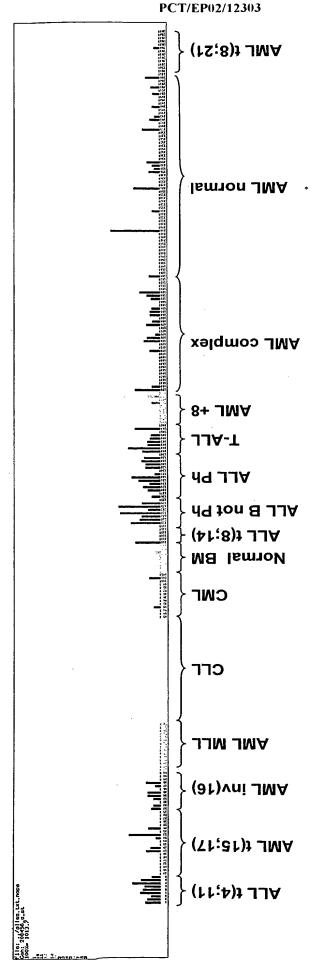
(L1;4)1 JJA

1

208456\_s\_at, RRAS2, CLL

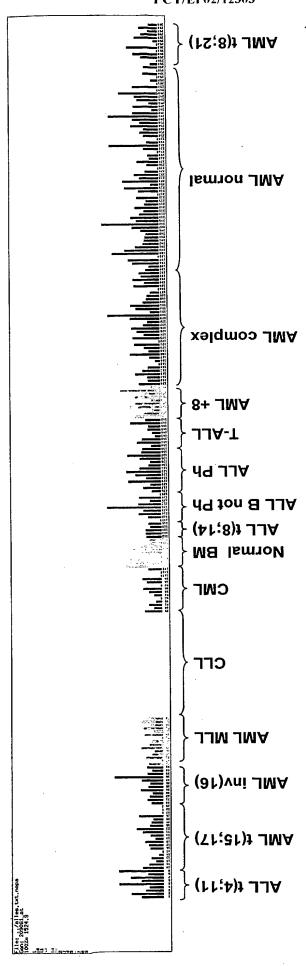


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209061\_at, NCOA3, CLL



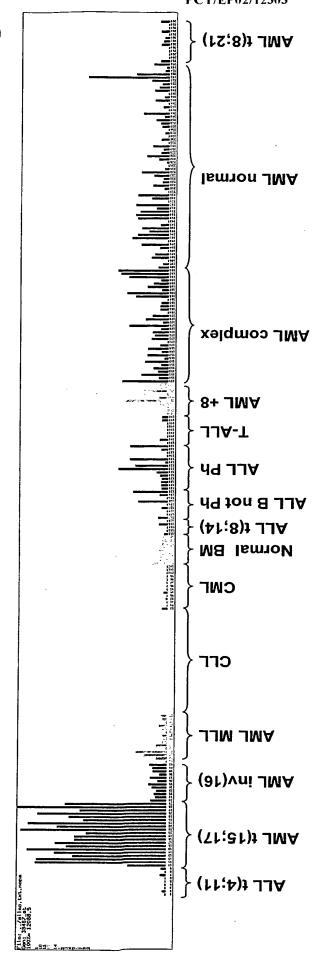


209374\_s\_at, IGHM, CLL

Figure 196

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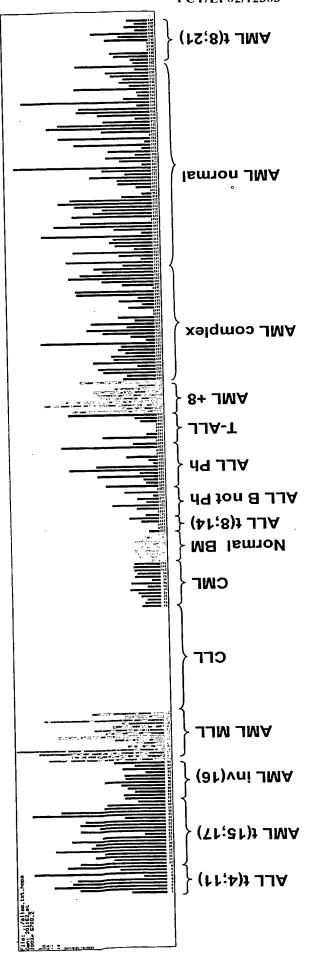




201162\_at, IGFBP7, CLL

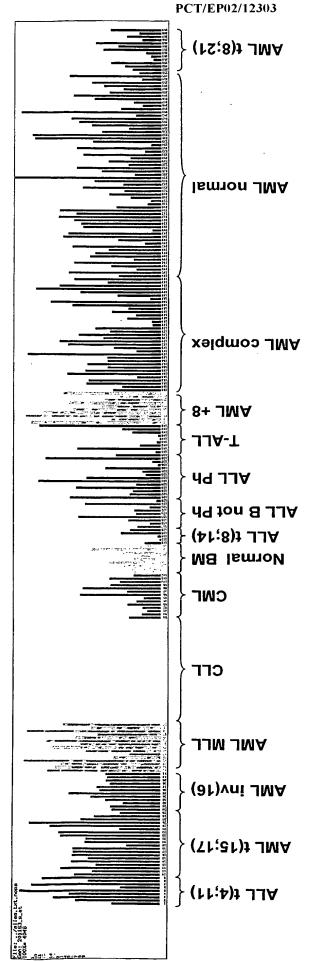
Figure 198

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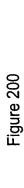


201163\_s\_at, IGFBP7, CLI

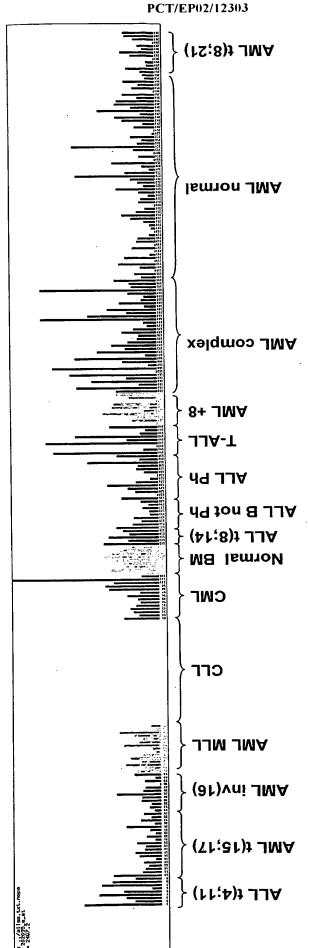
Figure 199







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201362\_at, NS1-BP, CML



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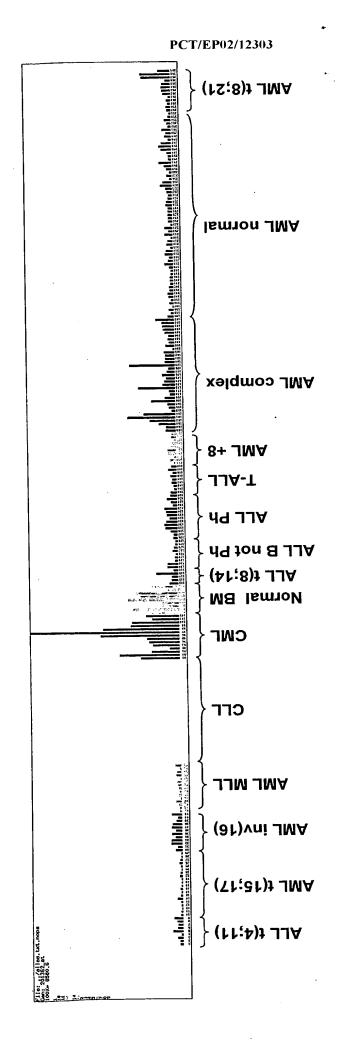
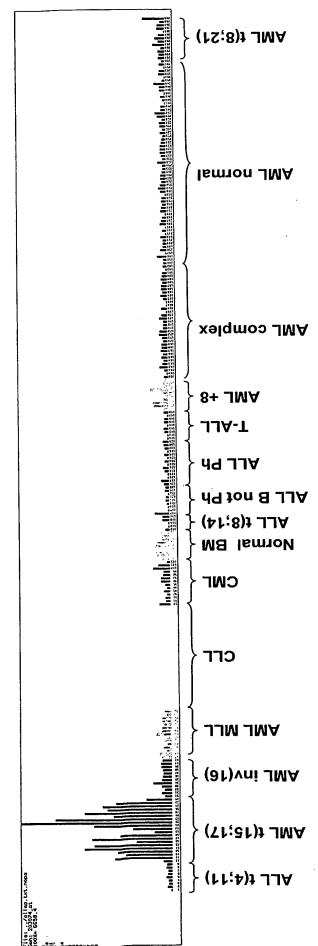
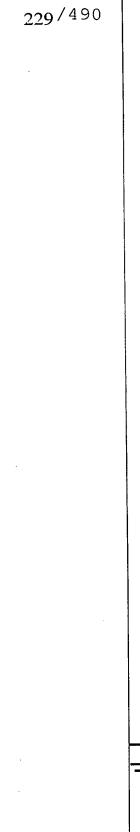
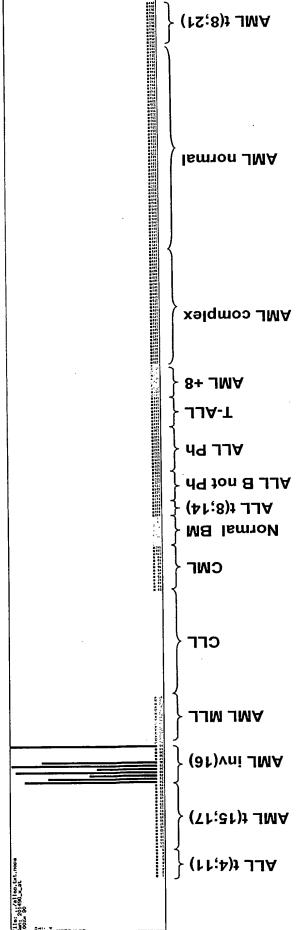


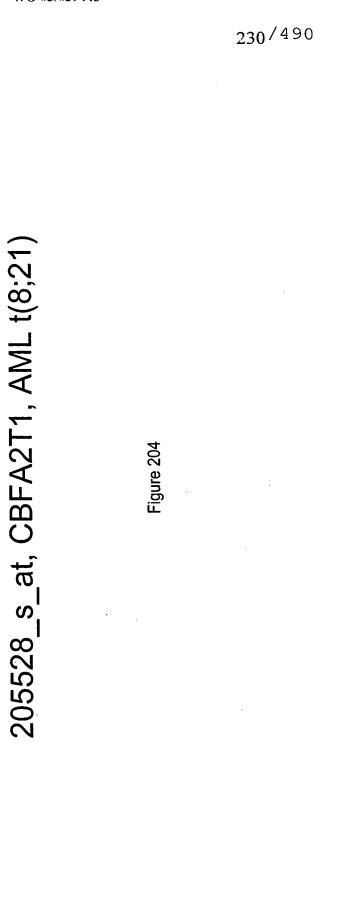


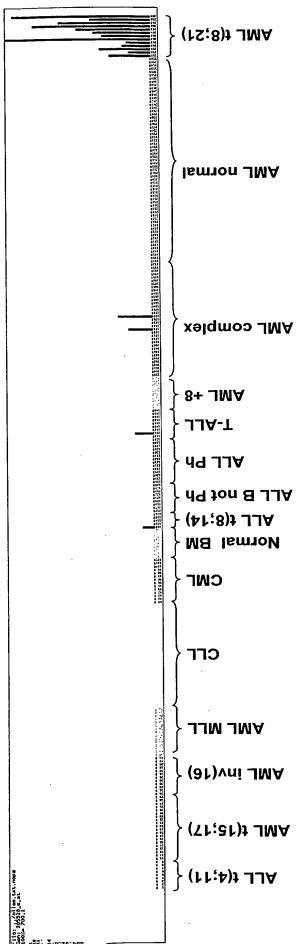
Figure 202



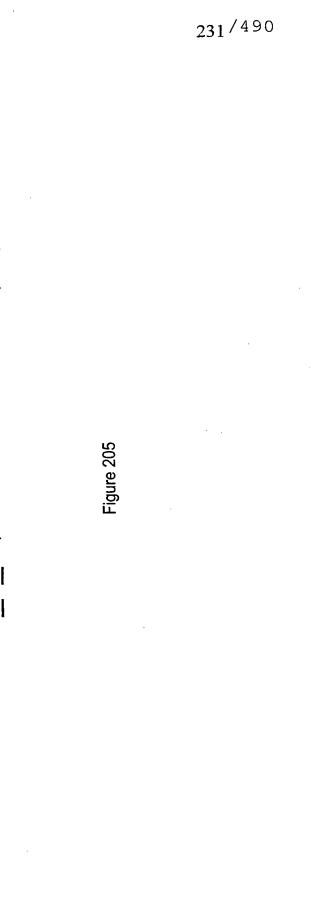


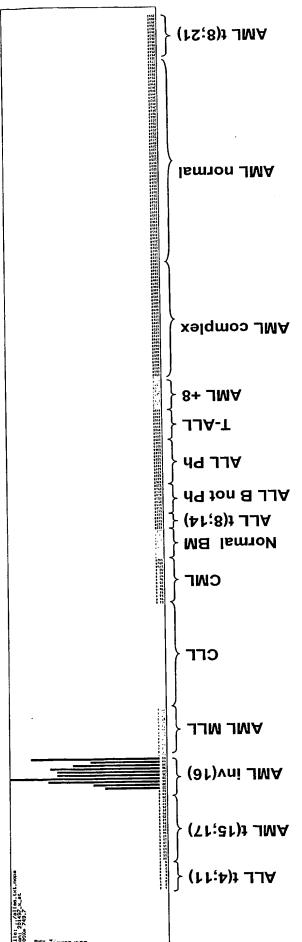




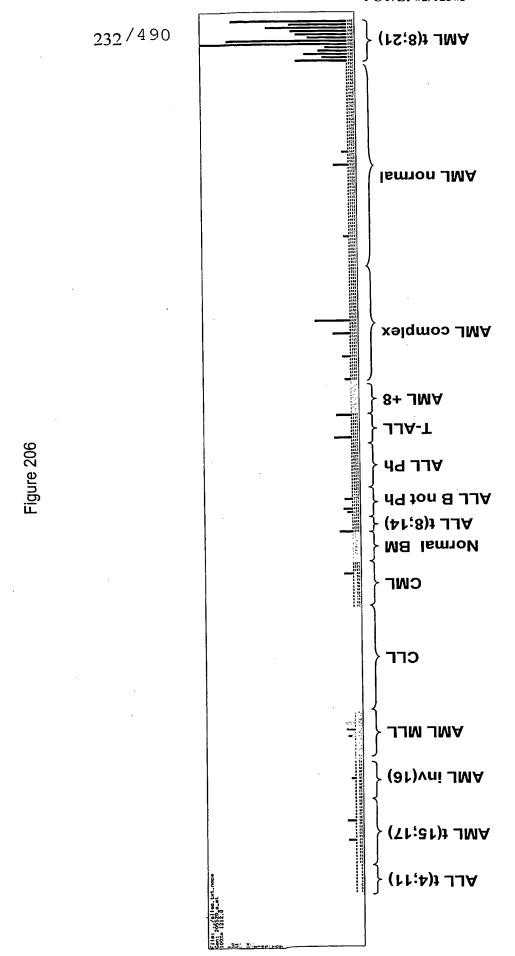


## 201497\_x\_at, MYH11, AML inv(16)

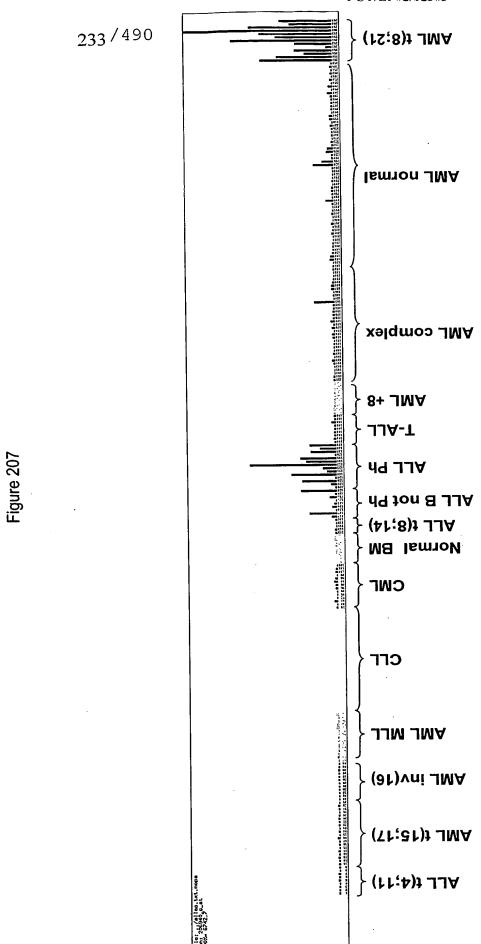








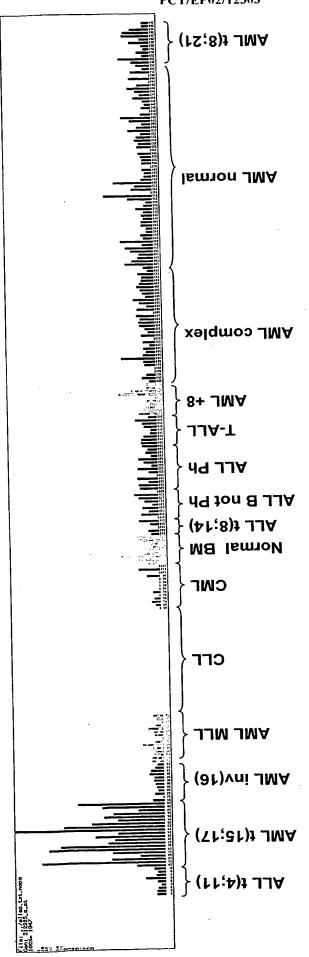




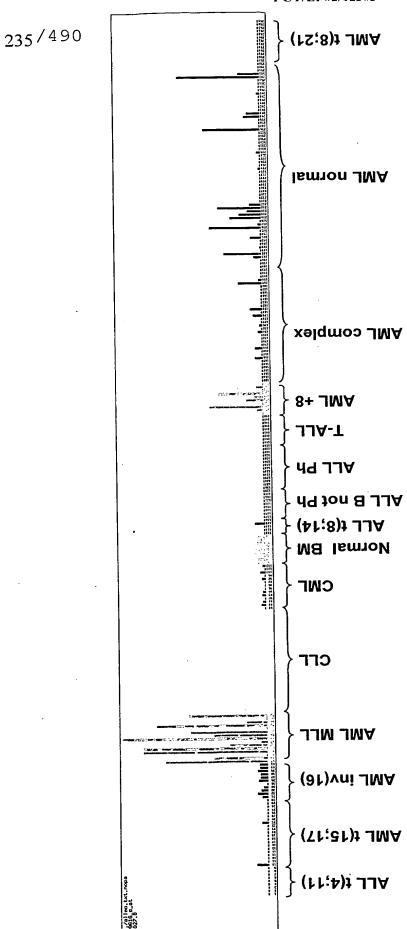
212285\_s\_at, AGRN, AML t(15;17)

Figure 208

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(91)vni JMA

(Tr;31)} JMA

} (\\\;\); \\



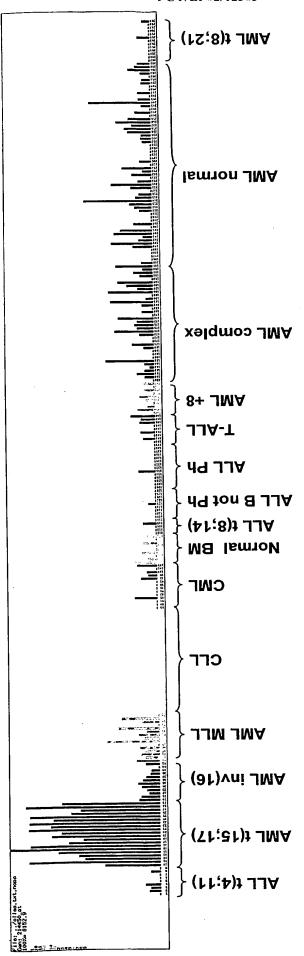
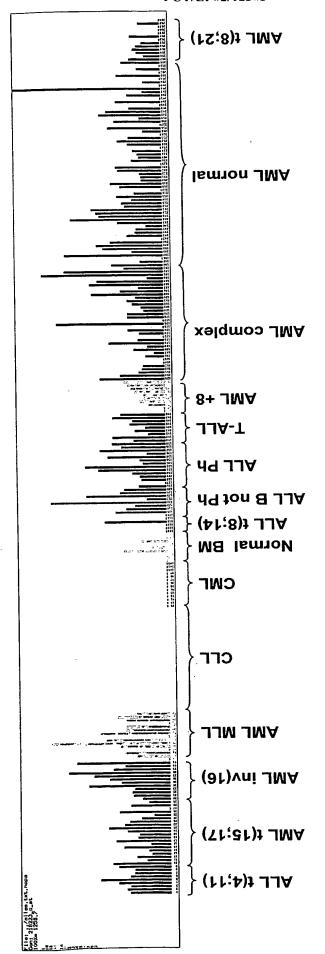


Figure 211

214450\_at, CTSW, AML t(15;17)

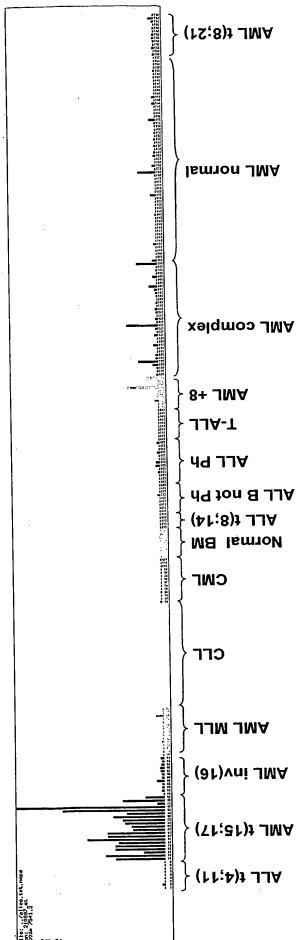


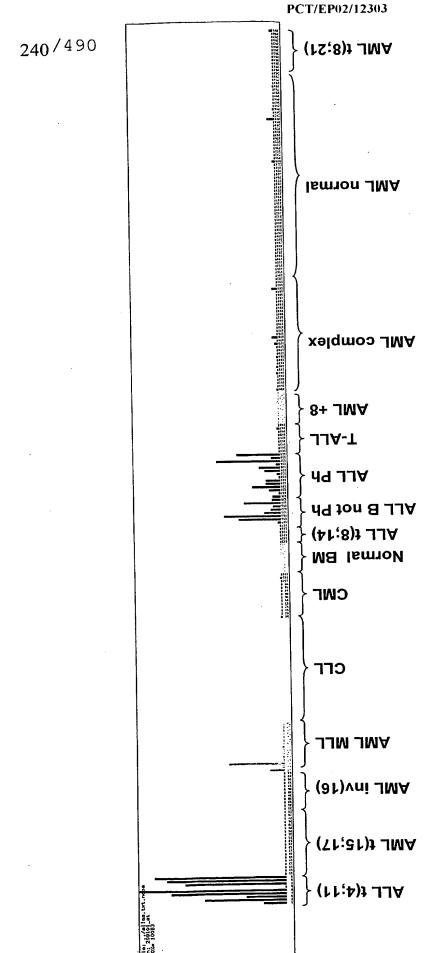


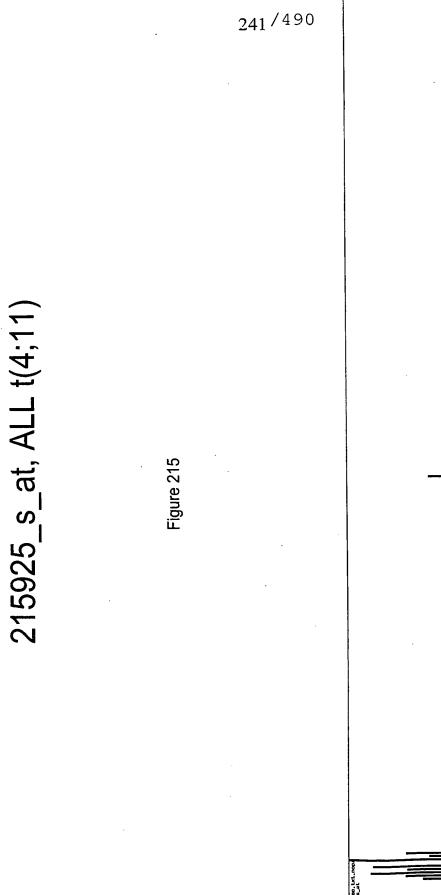


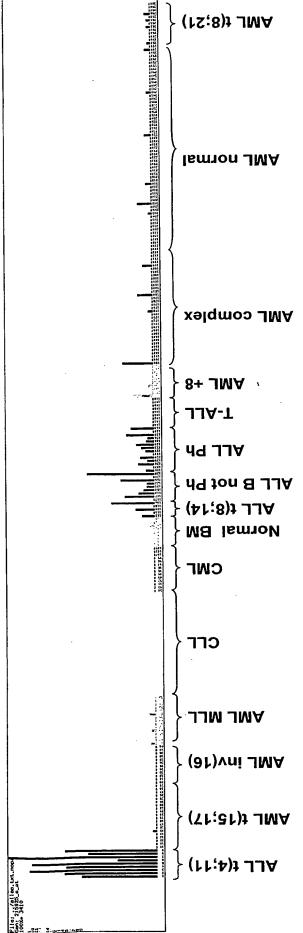








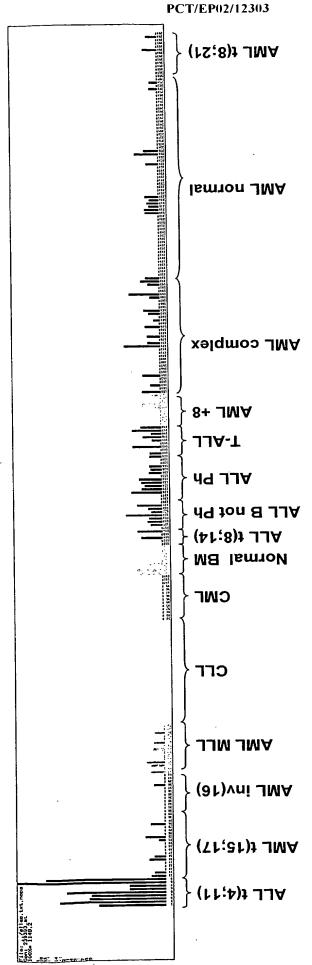




239393\_at, ALL t(4;11)



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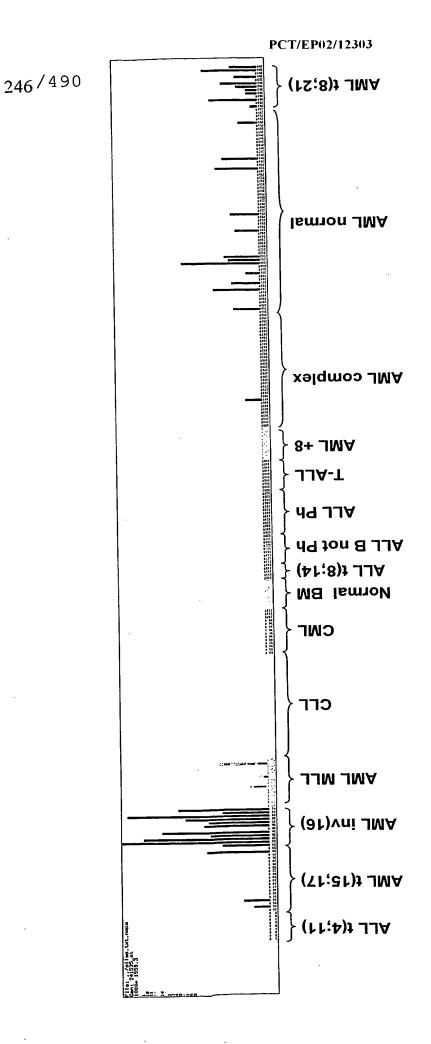


243/490 (12;8)3 JMA AML normal 239791\_at, HOXB6, AML normal, AML +8 **AML** complex 8+ JMA JJA-T Figure 217 ALL Ph ALL B not Ph (41;8)1 JJA Normal BM CWF CFF AML MLL (8t)vni JMA (Tr;2r)3 JMA (L1;4)) JJA

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240581\_at, ALL t(4;11)

PCT/EP02/12303

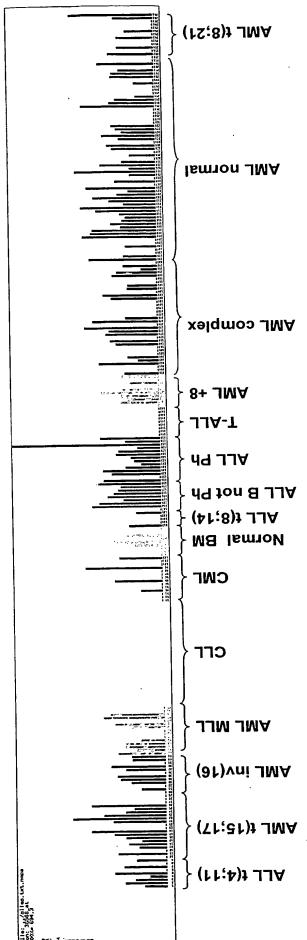


(rt;4)1 JJA

36566\_at, CTNS, T-ALL



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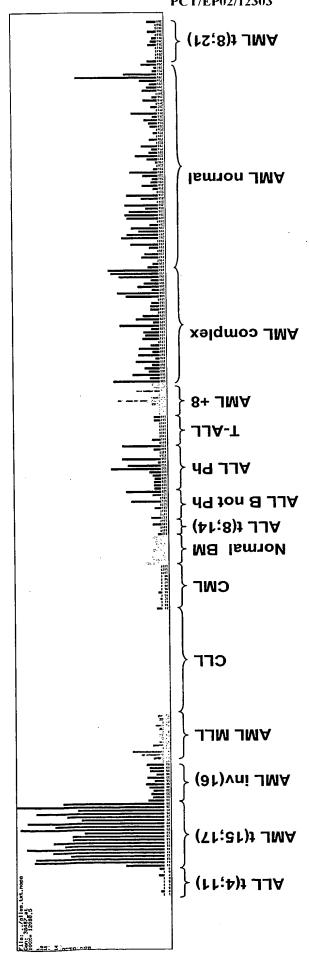
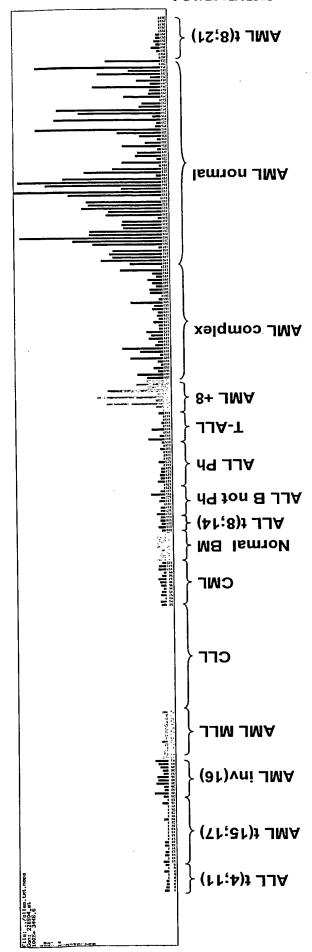




Figure 224

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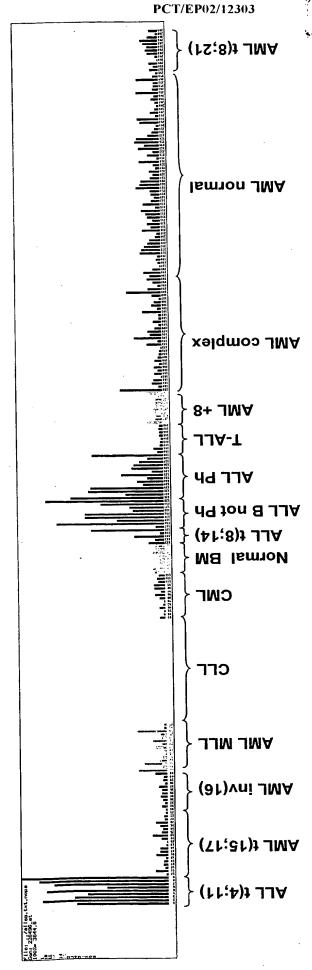
228904\_at, AML normal, AML +8, AML complex

Figure 22

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226496\_at, ALL, CL

Figure 227



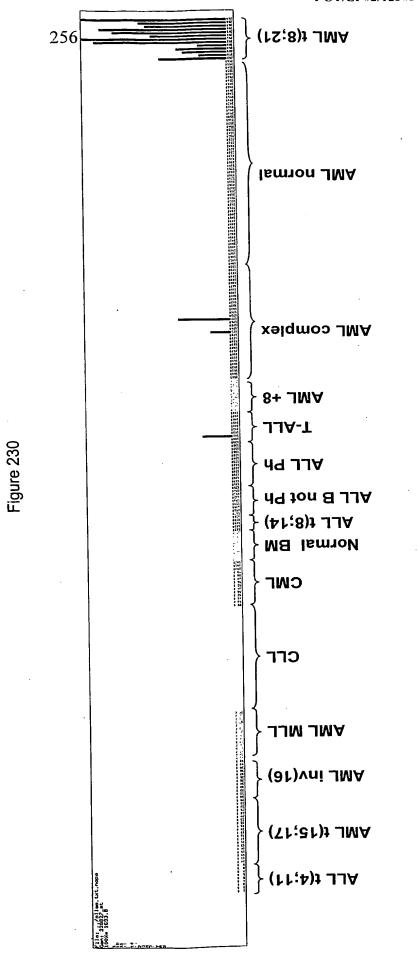
**AML MLL** 

(81)vni JMA

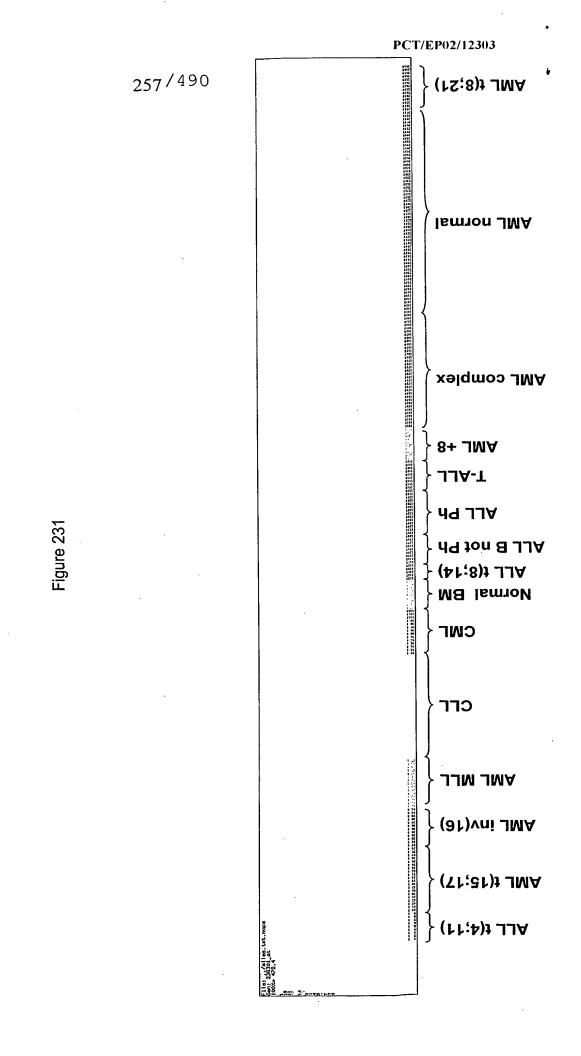
(\times\time

(11;4)J JJA





....

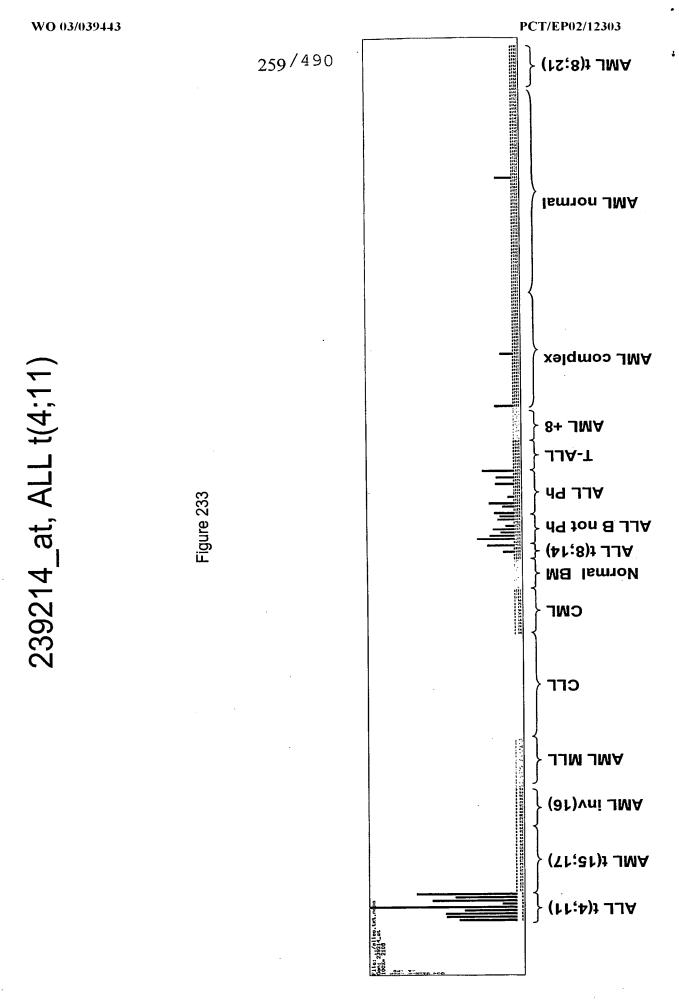


WO 03/039443

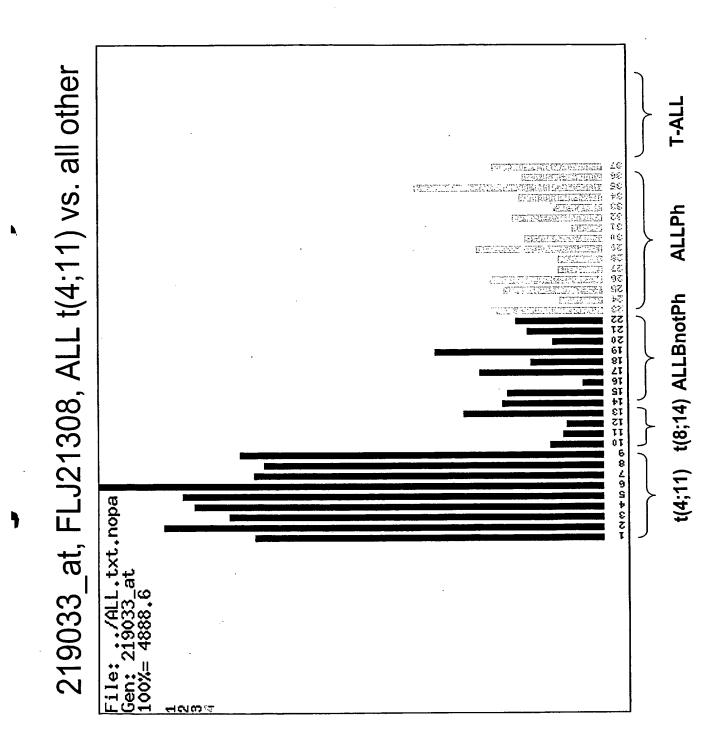
236301\_at, CLL

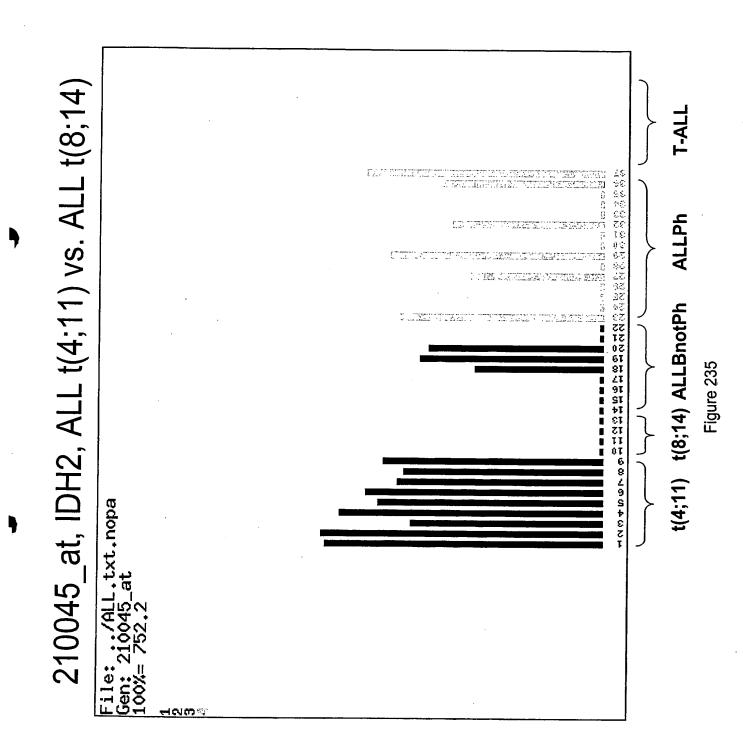
(T1;31)) JMA

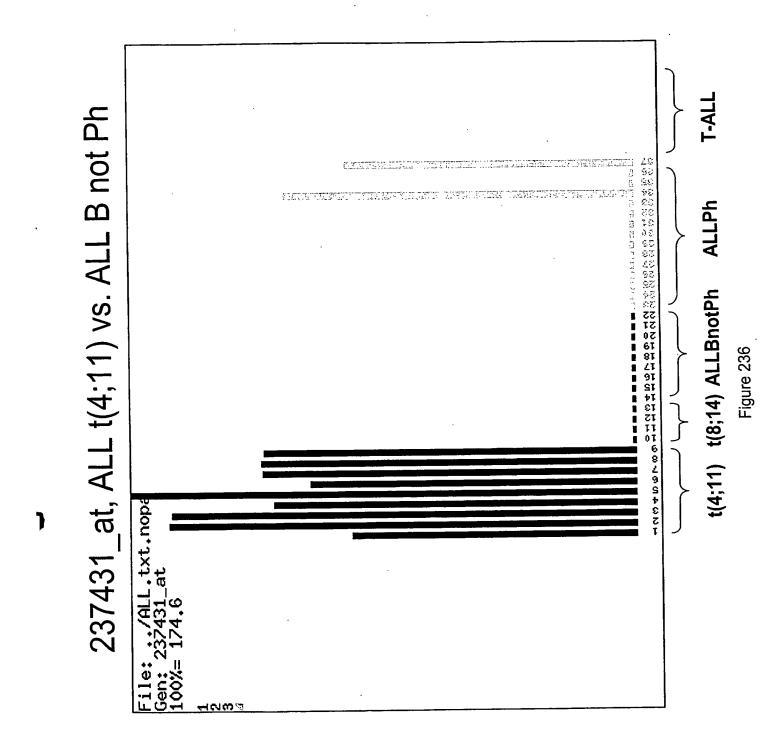
(Lt;4)} JJA

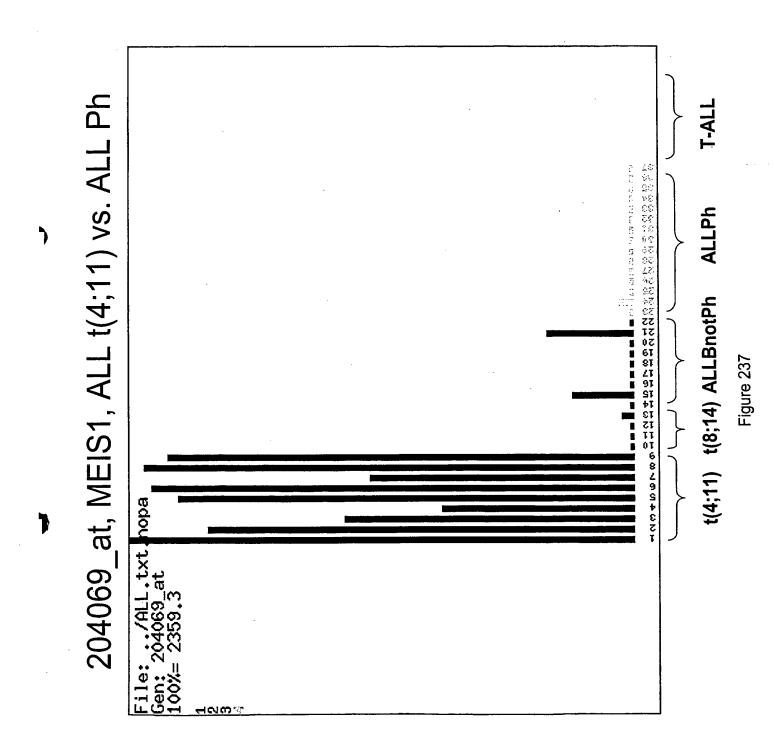


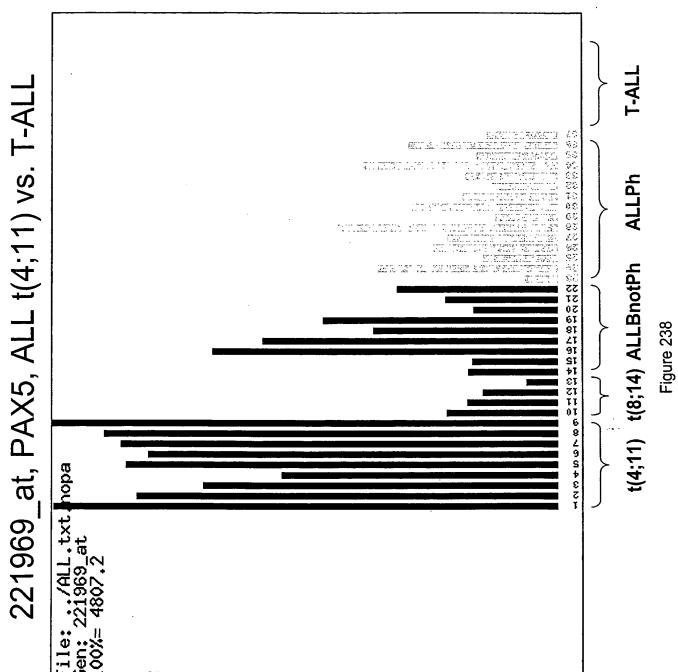




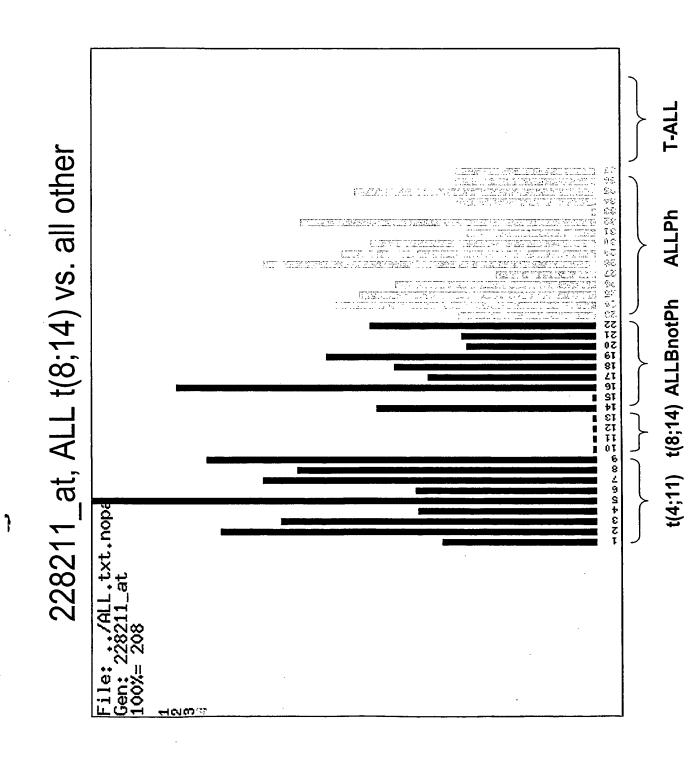


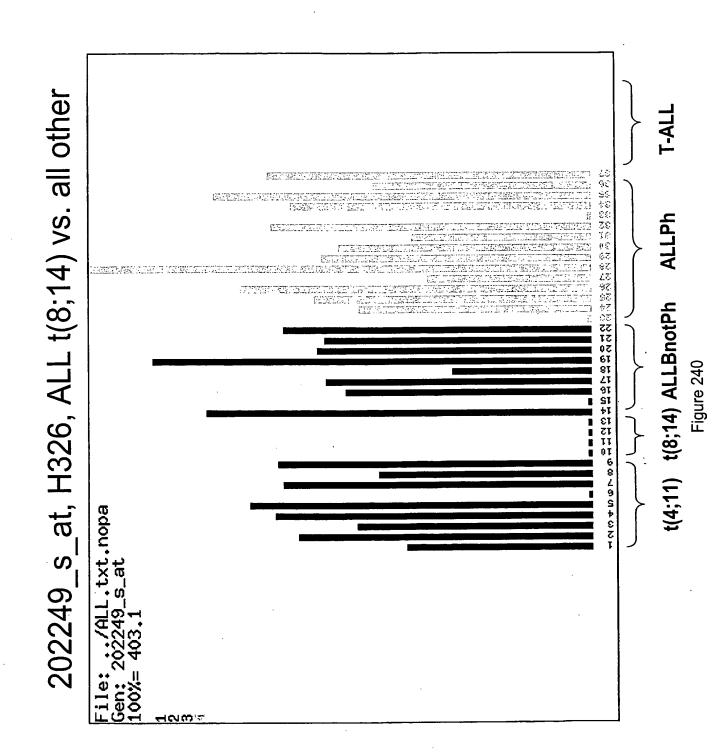


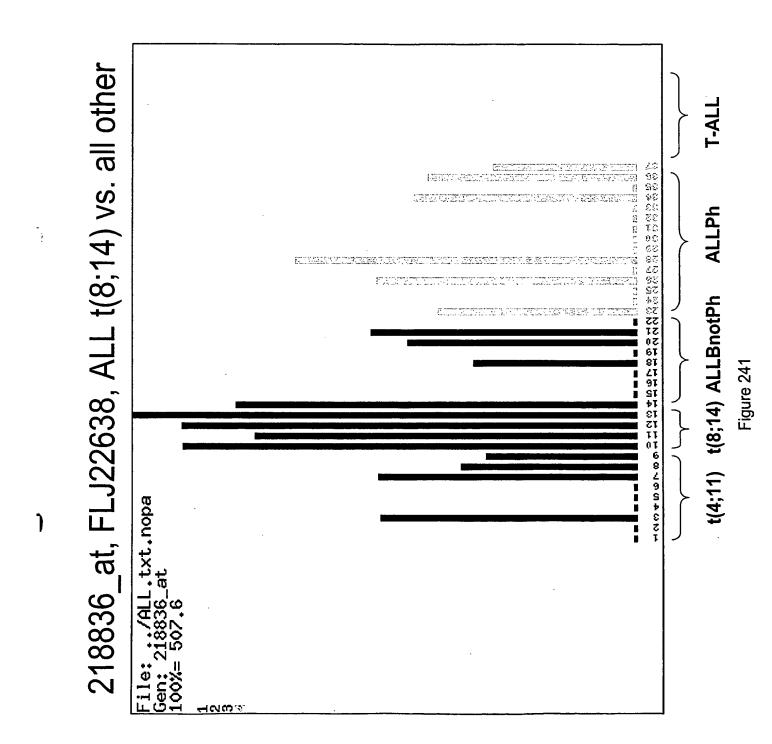


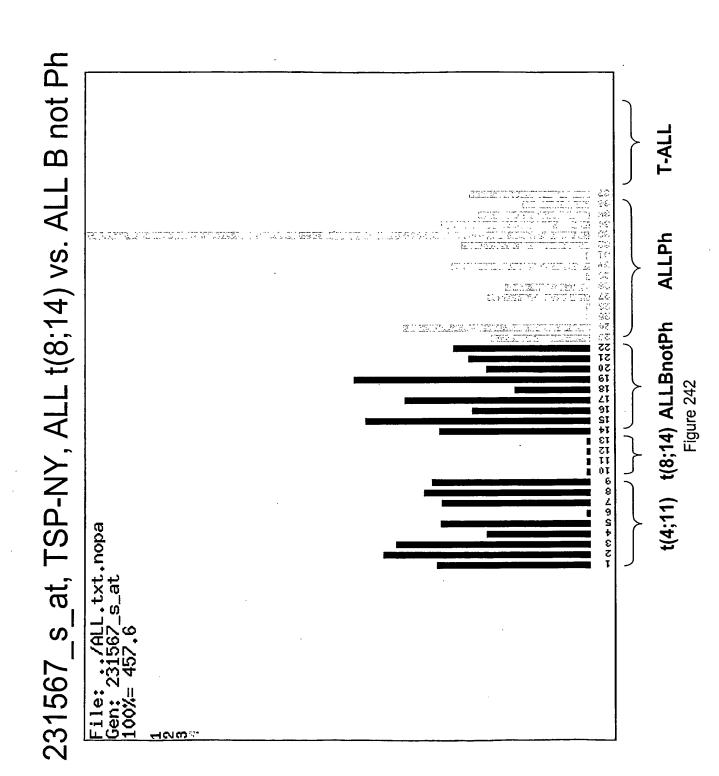




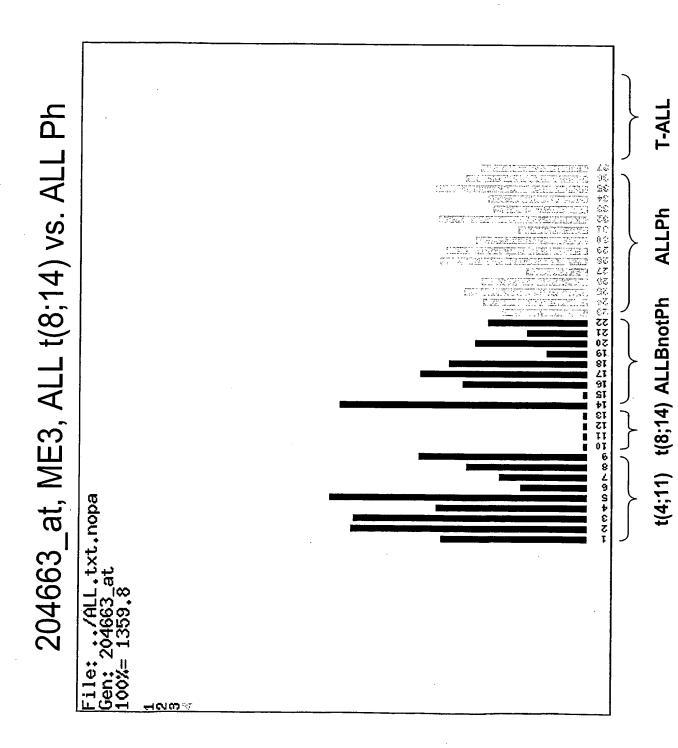


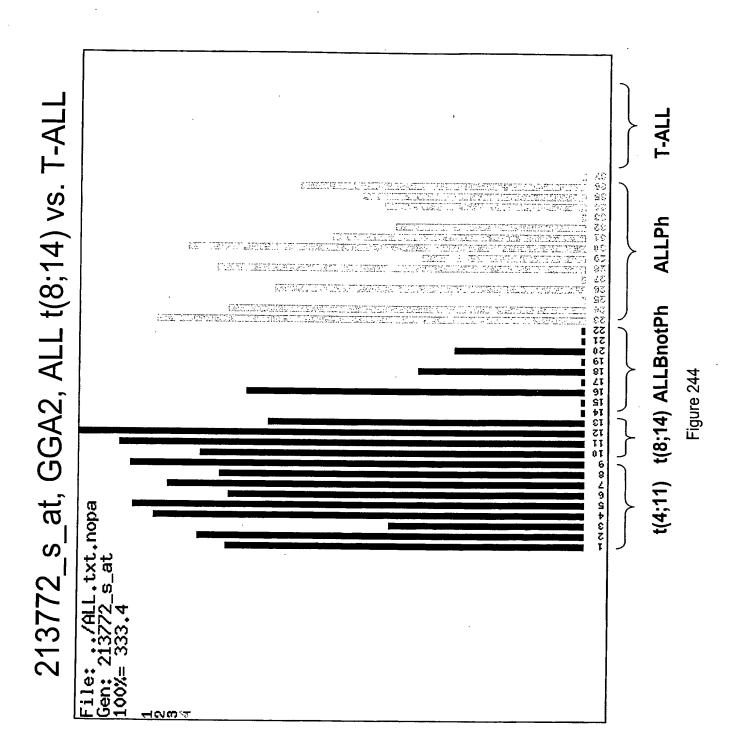




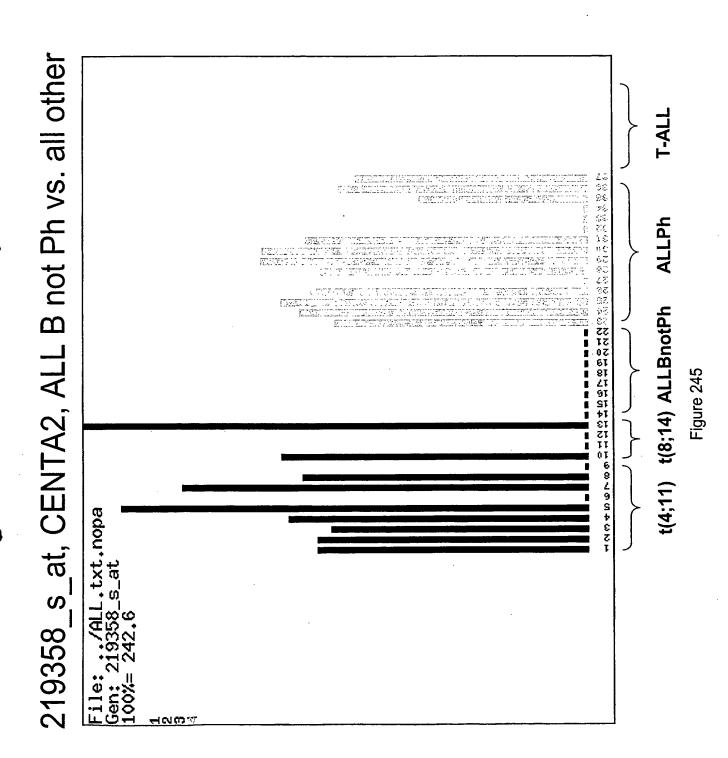




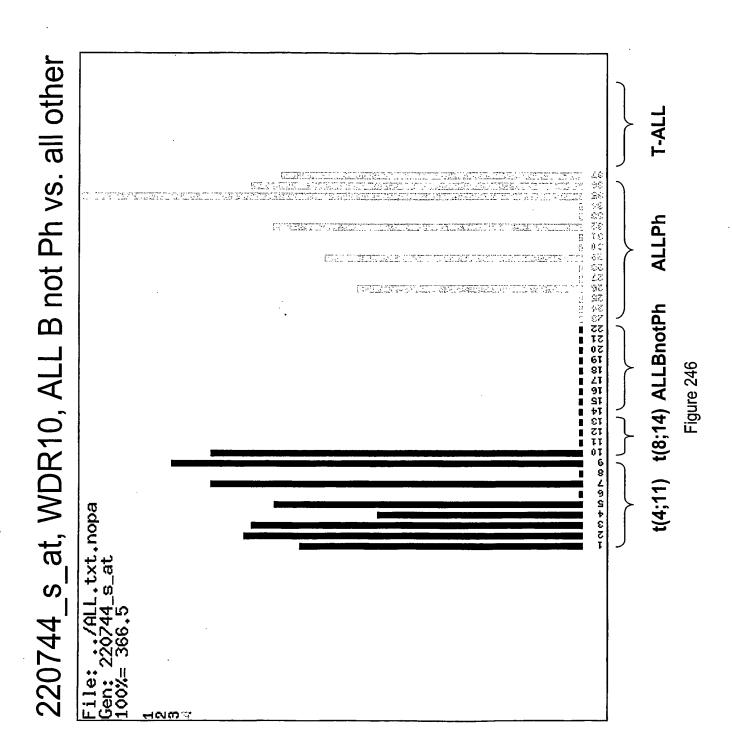


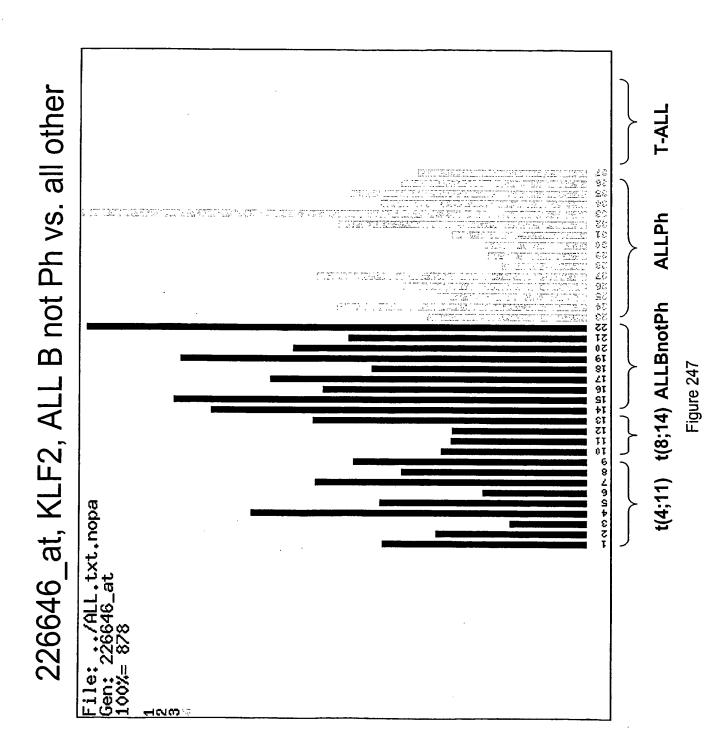


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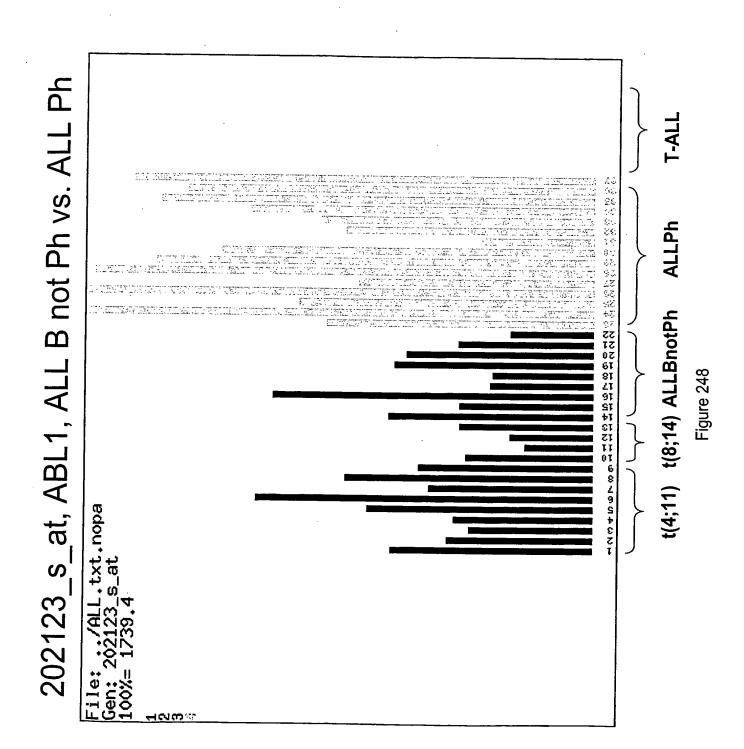


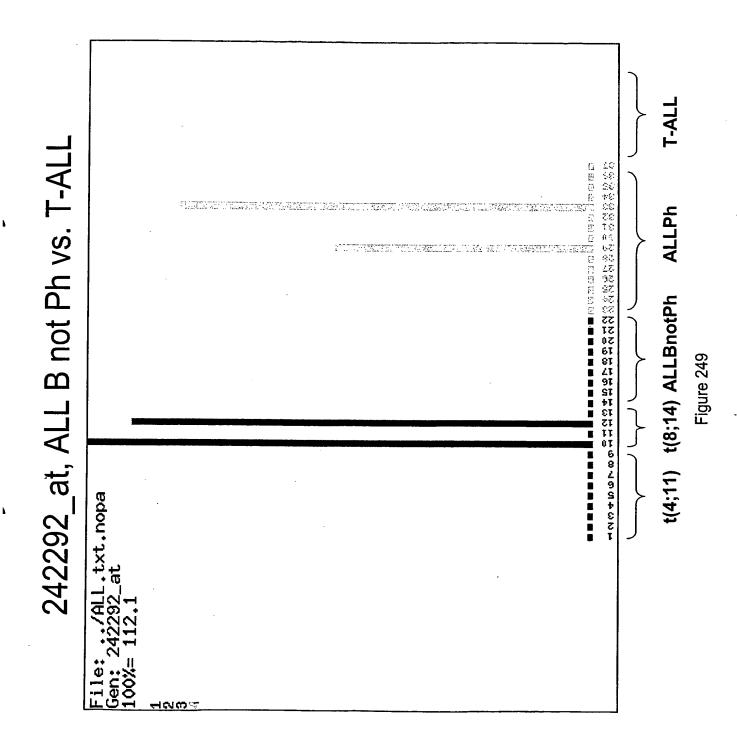
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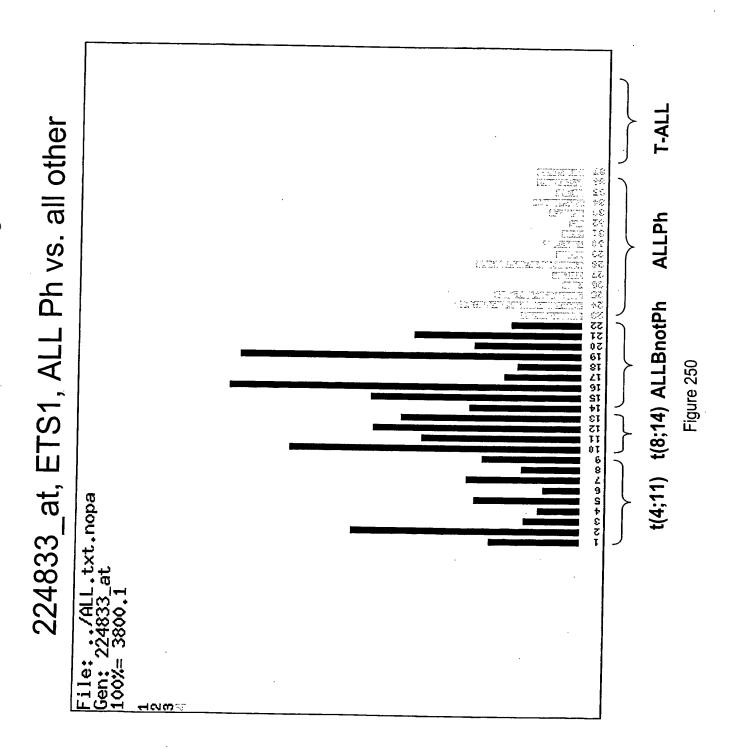


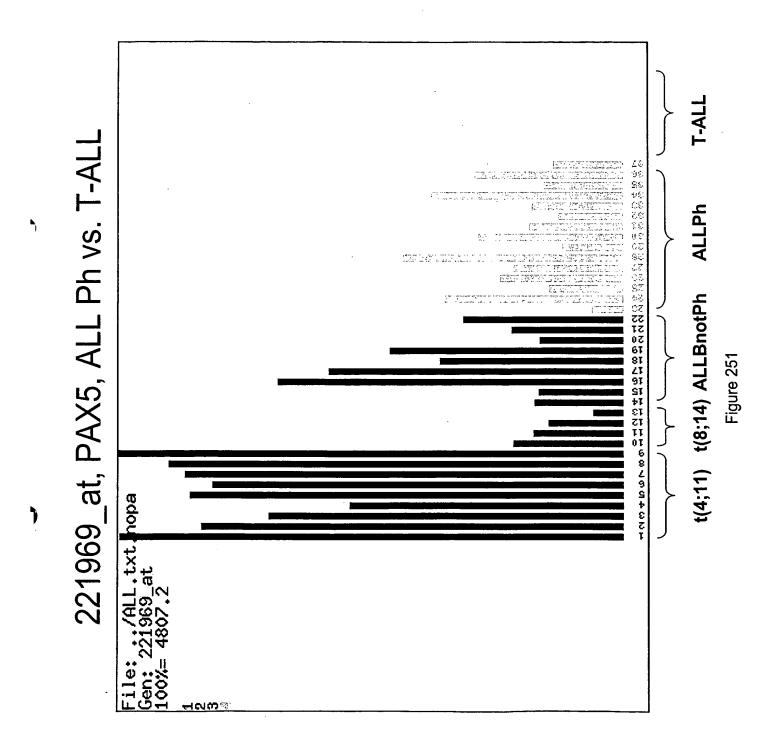


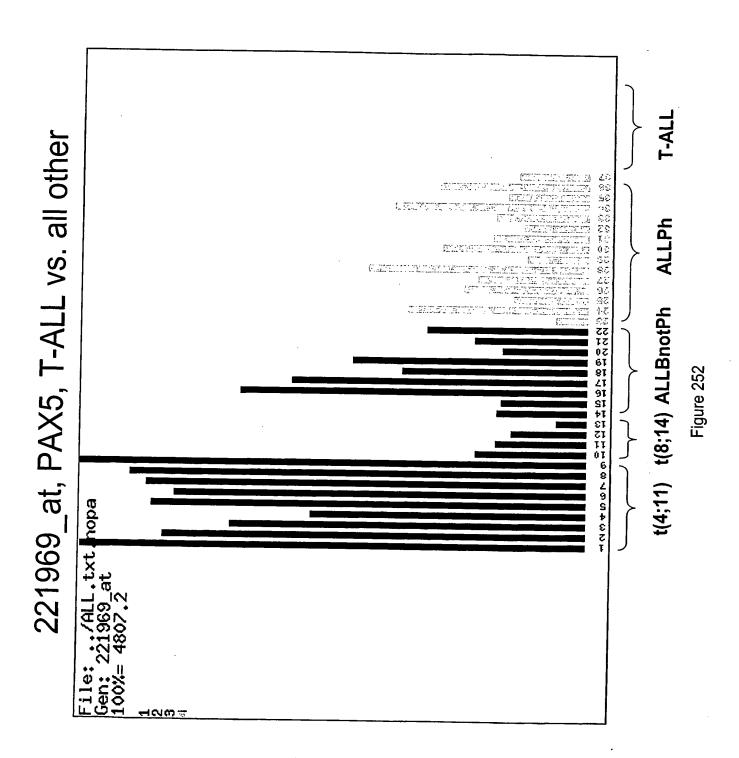
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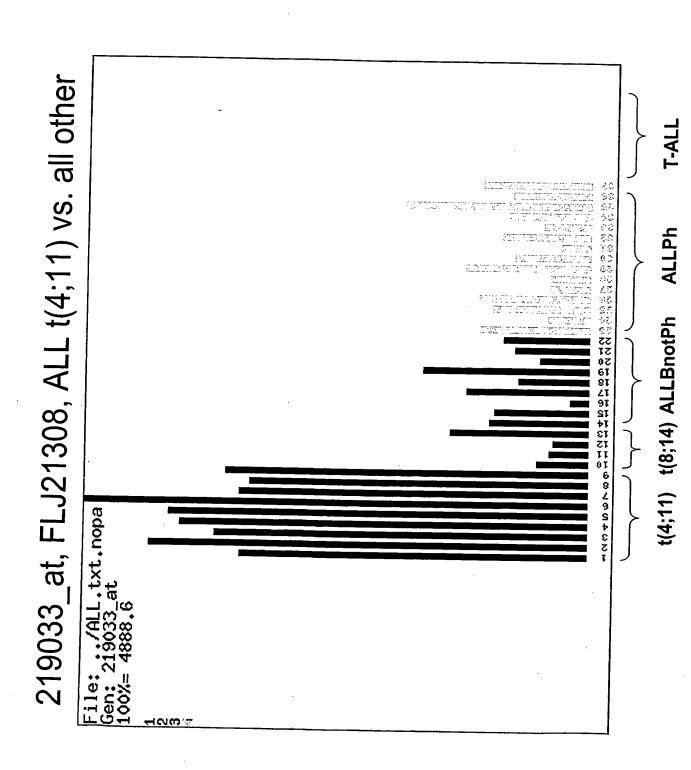
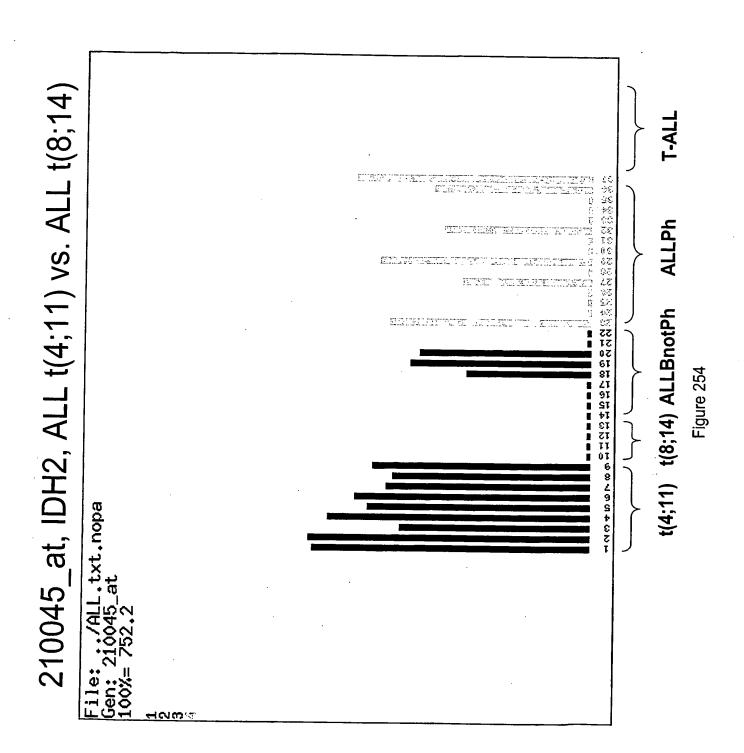
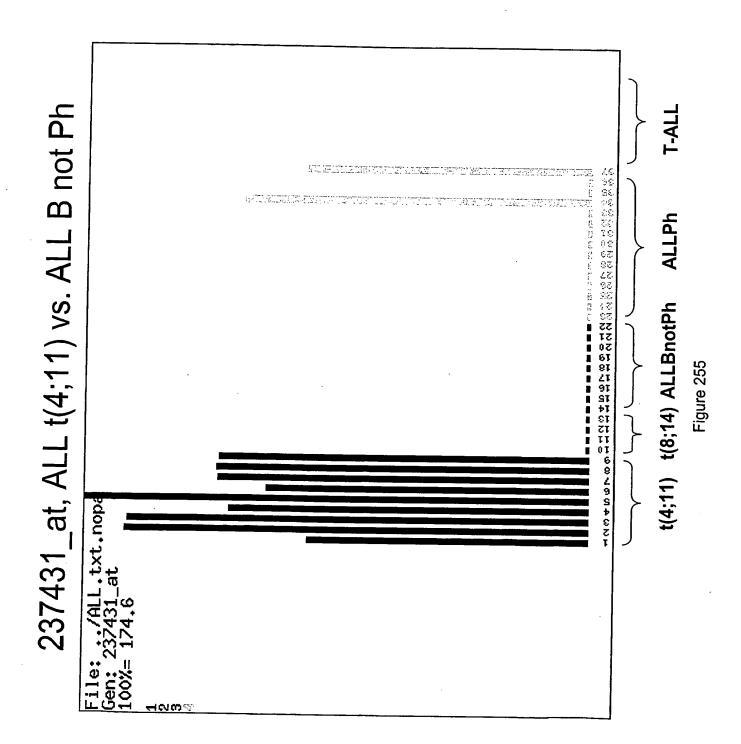
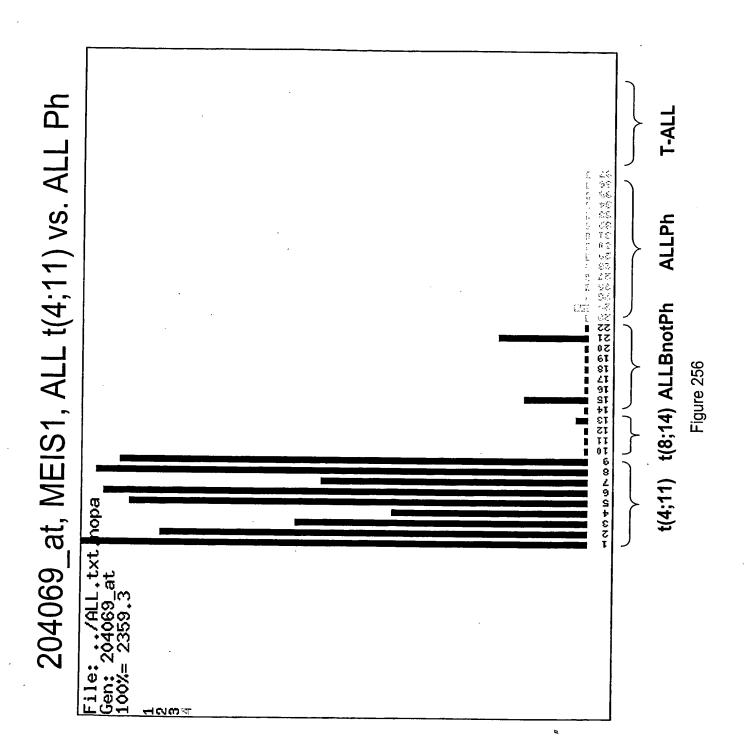
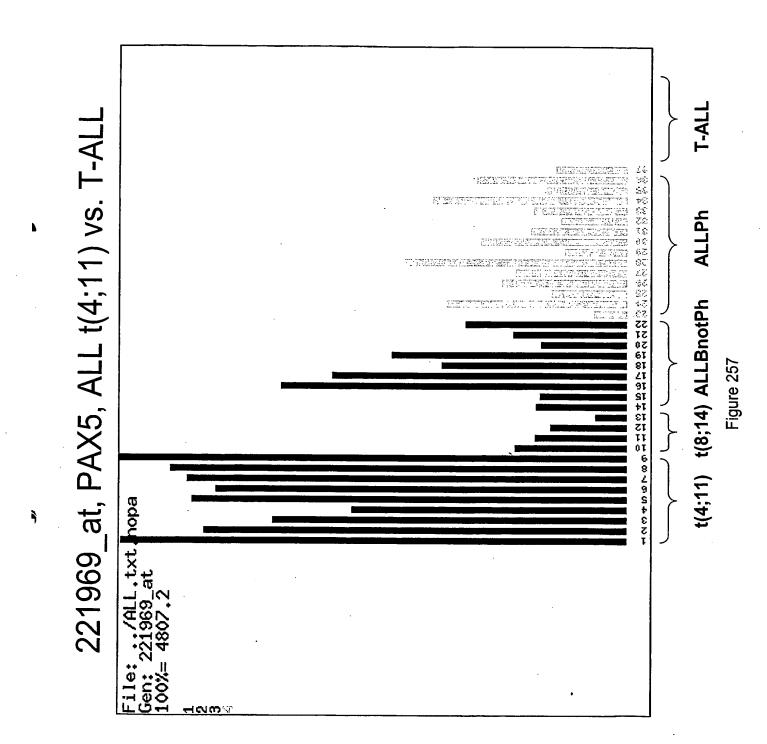


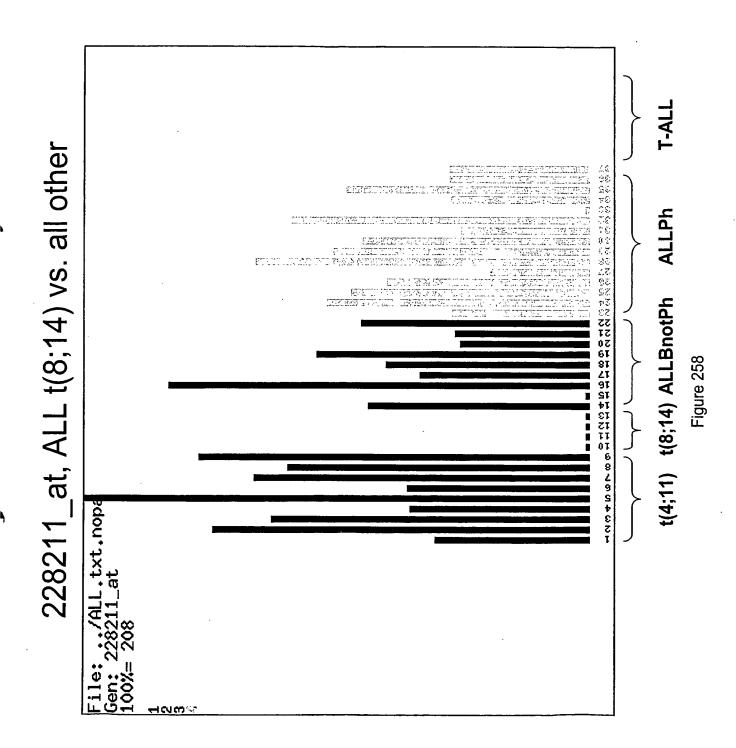
Figure 253



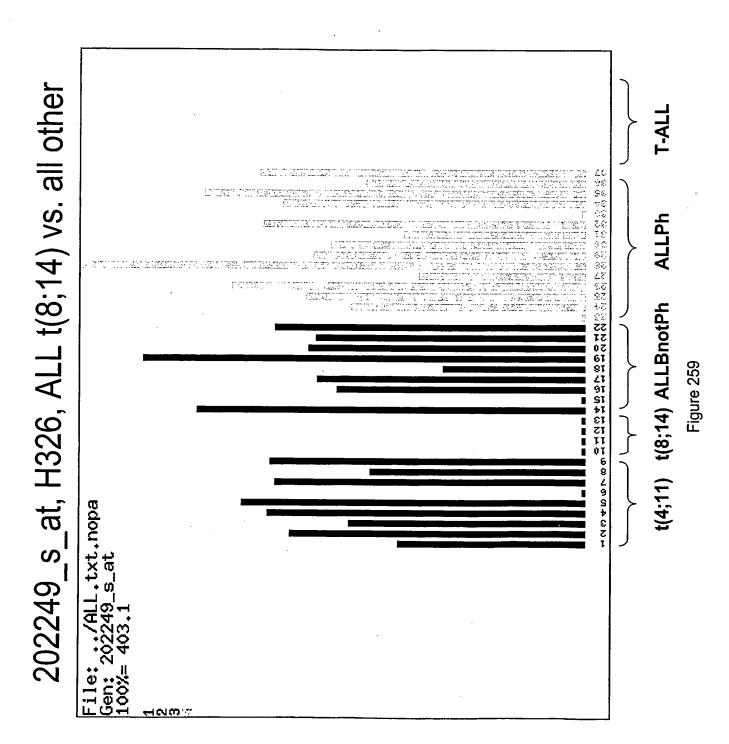


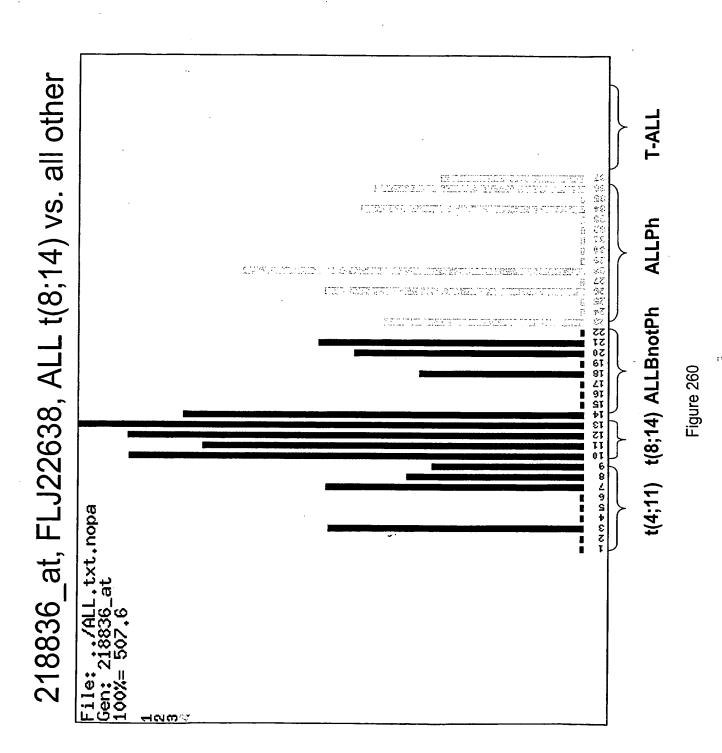


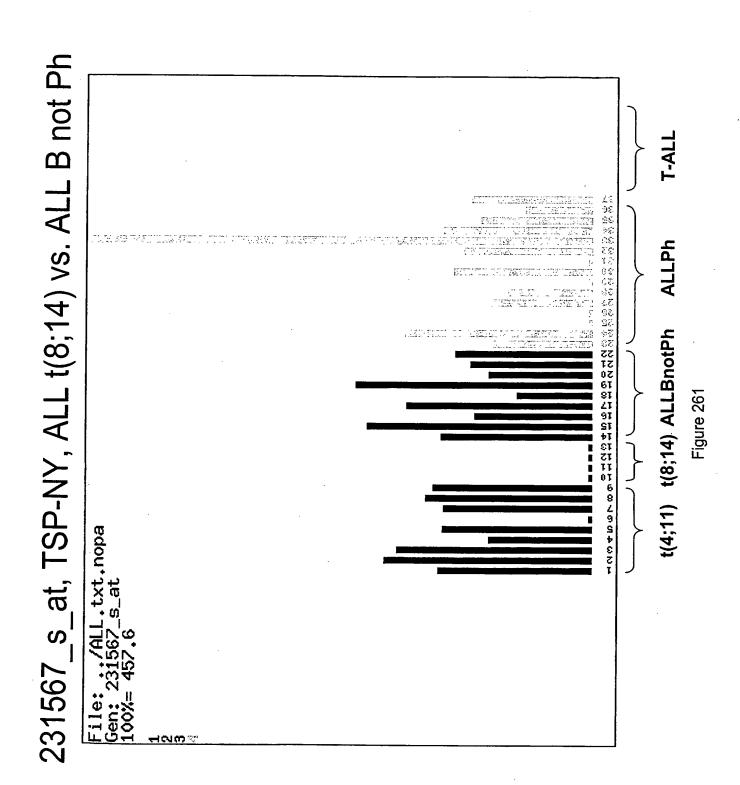


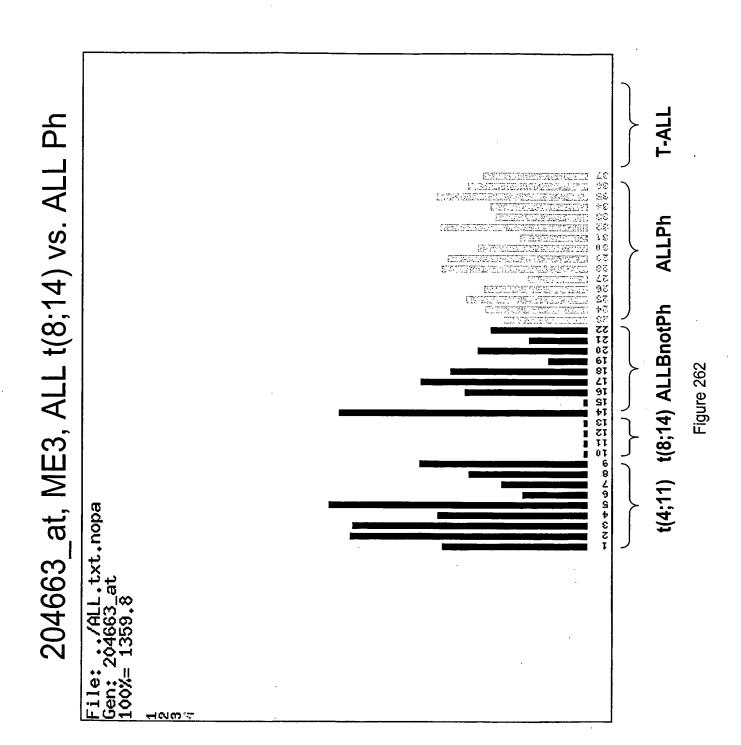


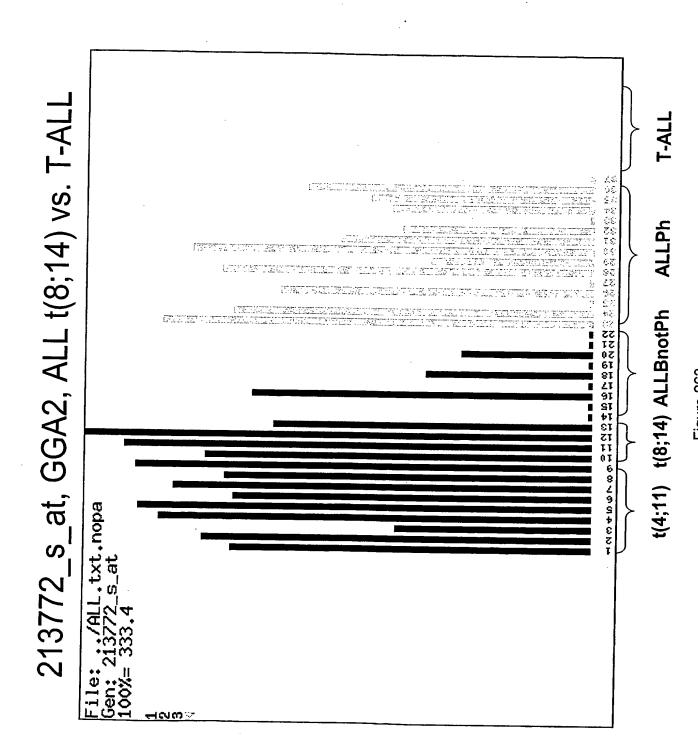
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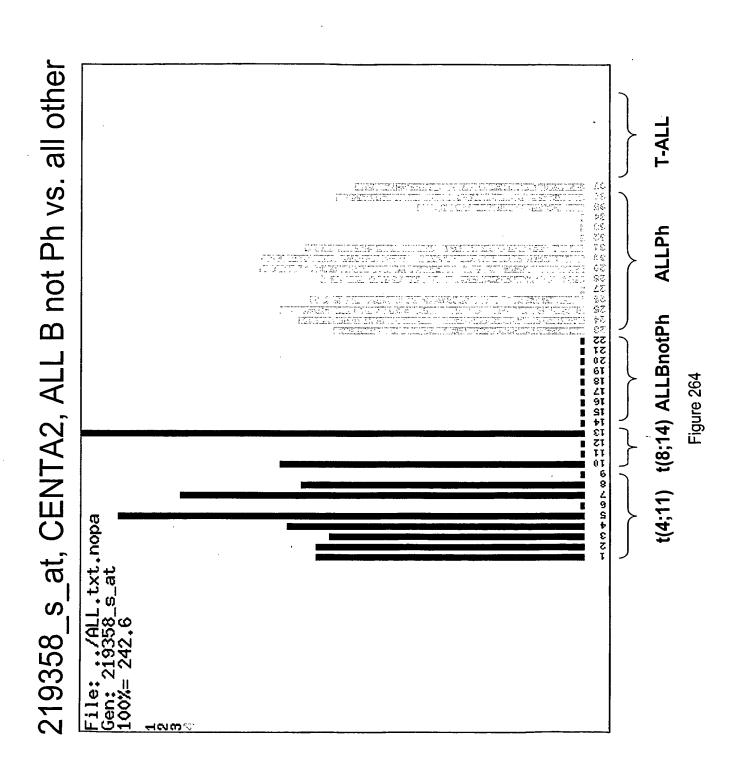


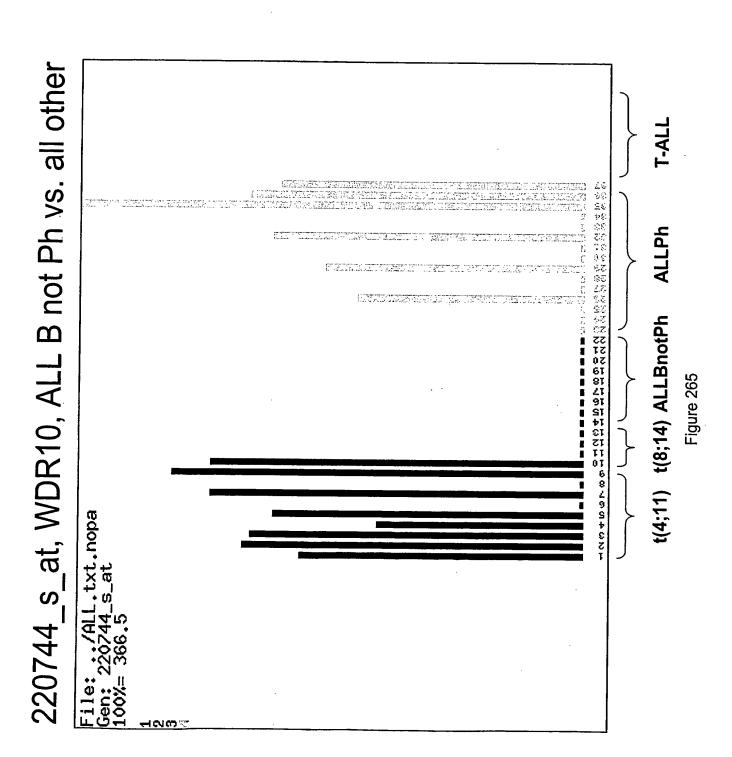


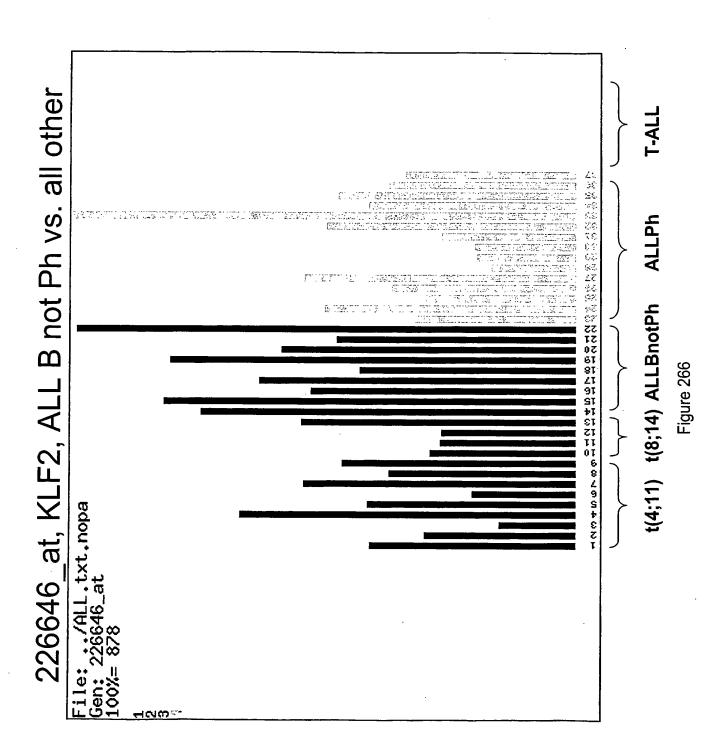


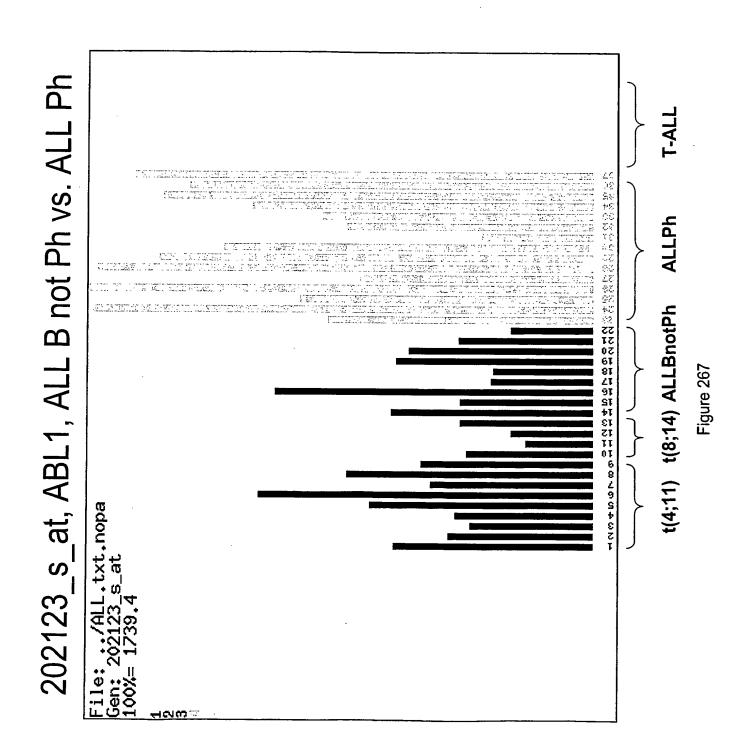


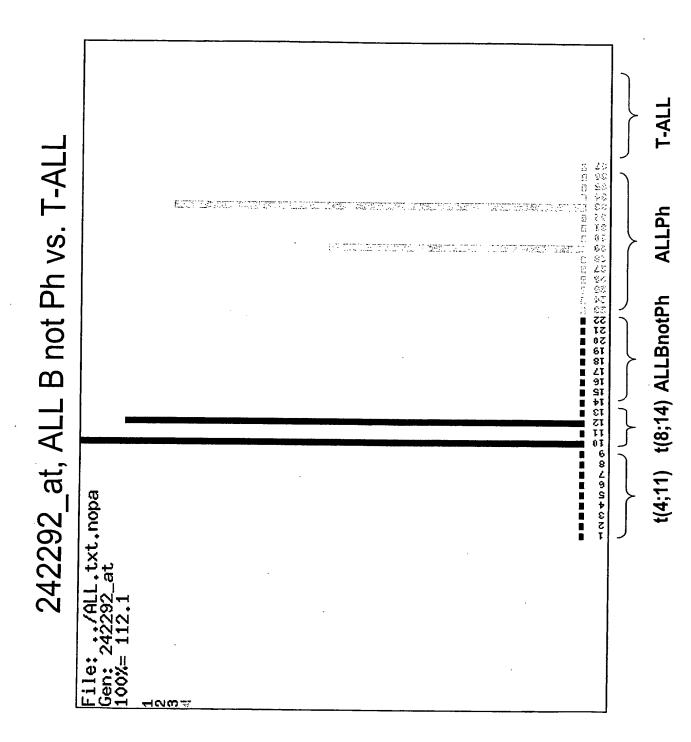
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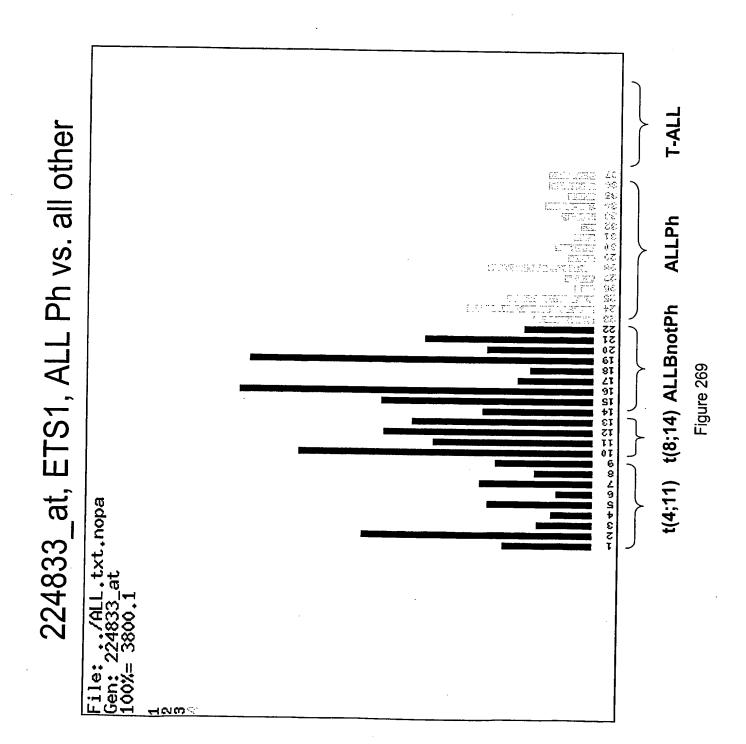


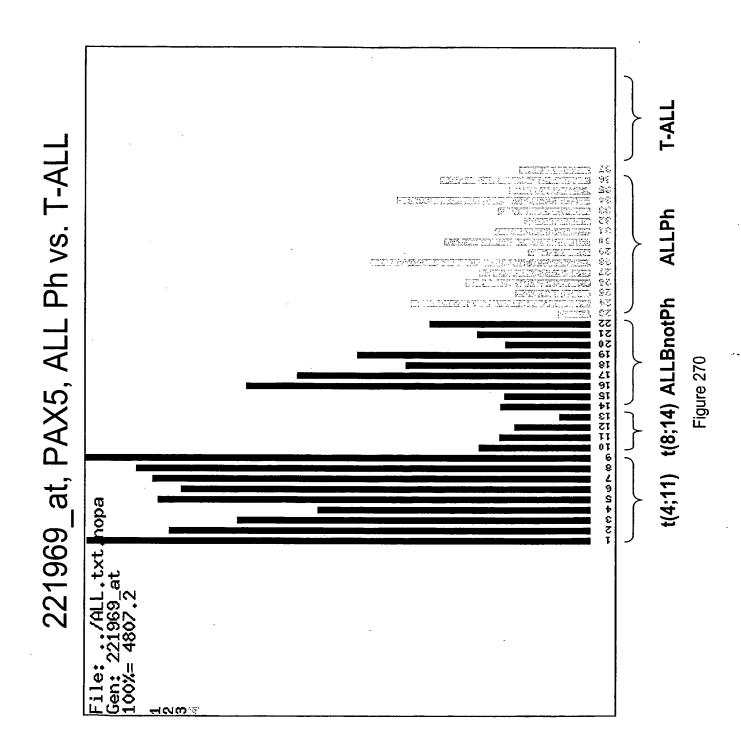


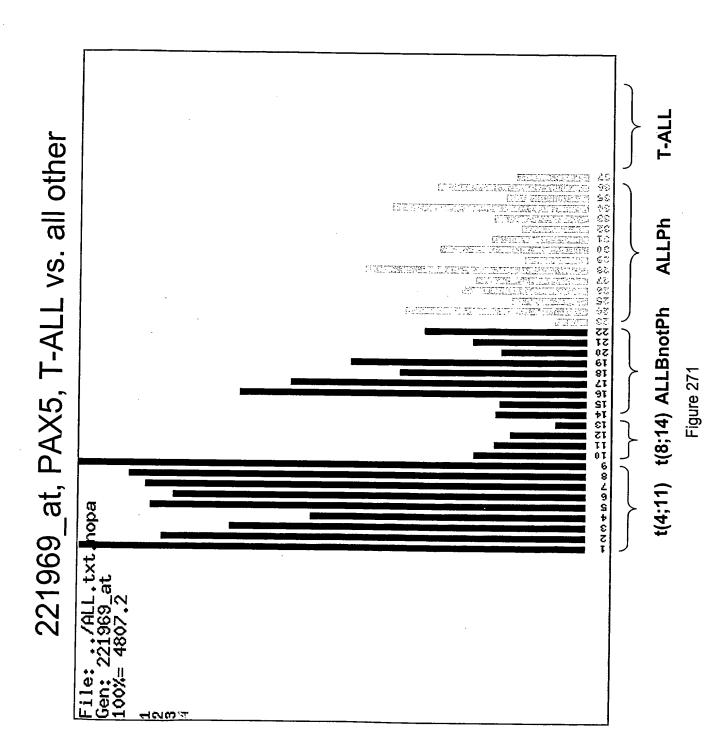




igure 268



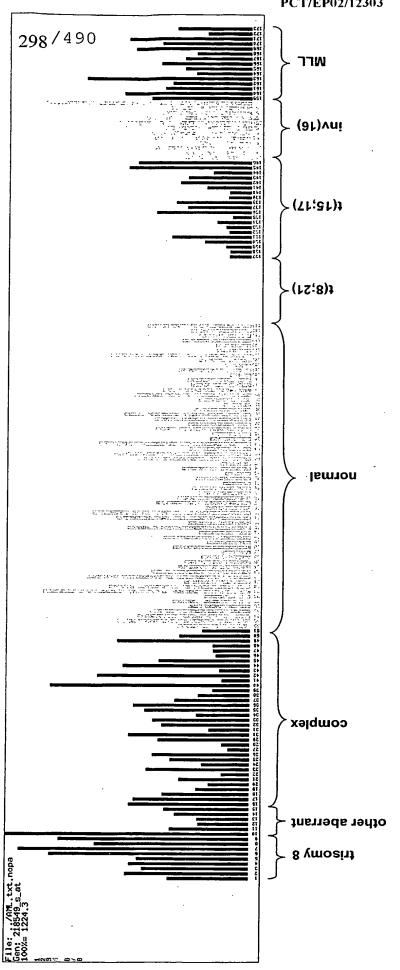




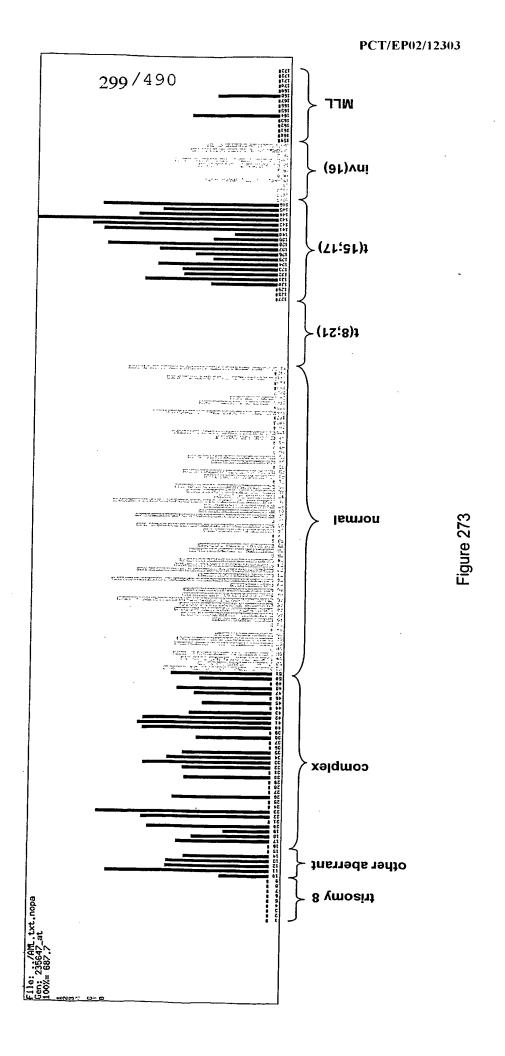
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## 218549\_s\_at, LOC51115, trisomy 8 vs. other aberrant

Figure 272

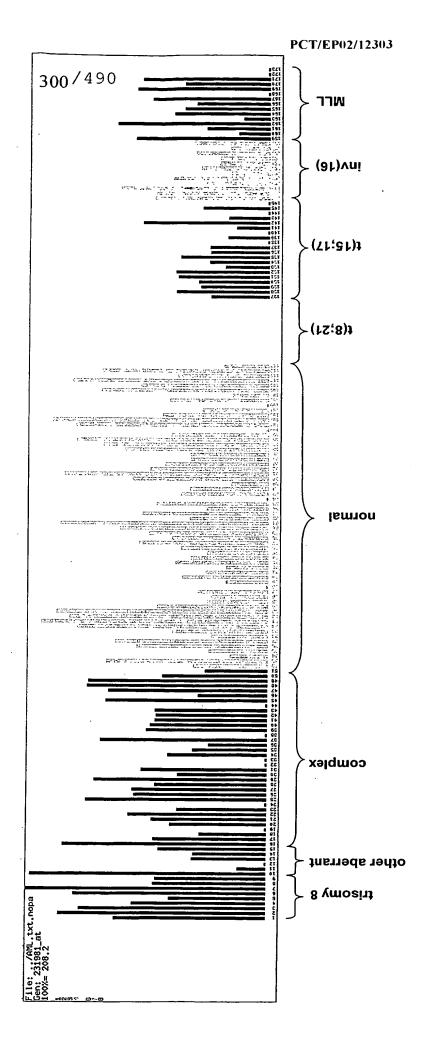


235647\_at, trisomy 8 vs. all other AMI

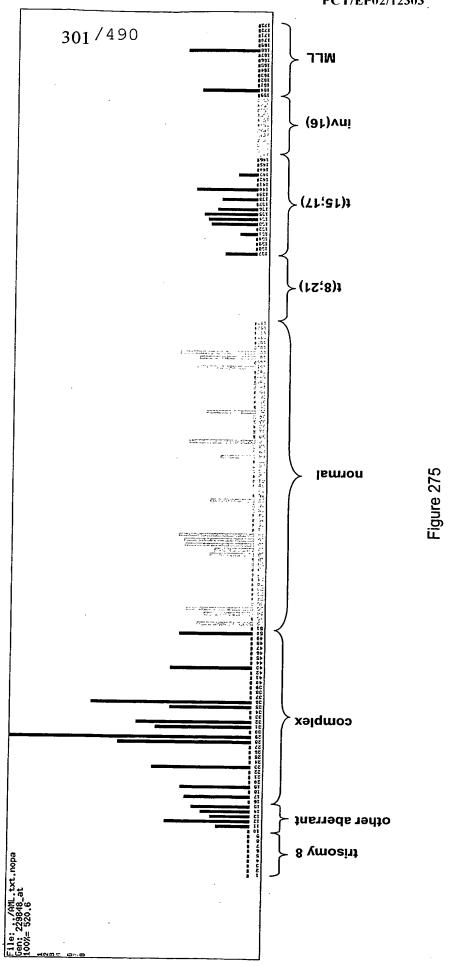


231981\_at, trisomy 8 vs. all other AML

Figure 274



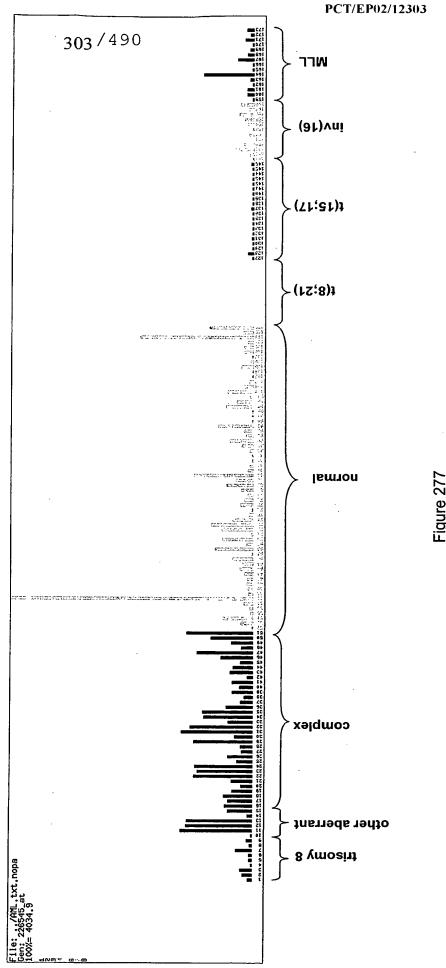
229848\_at, ZNF10, trisomy 8 vs. ather aberrant



212586\_at, ARTS-1, trisomy 8 vs. complex

302/490 NTL (at)vni (15;17) t(8;21)normal complex other aberrant trisomy 8

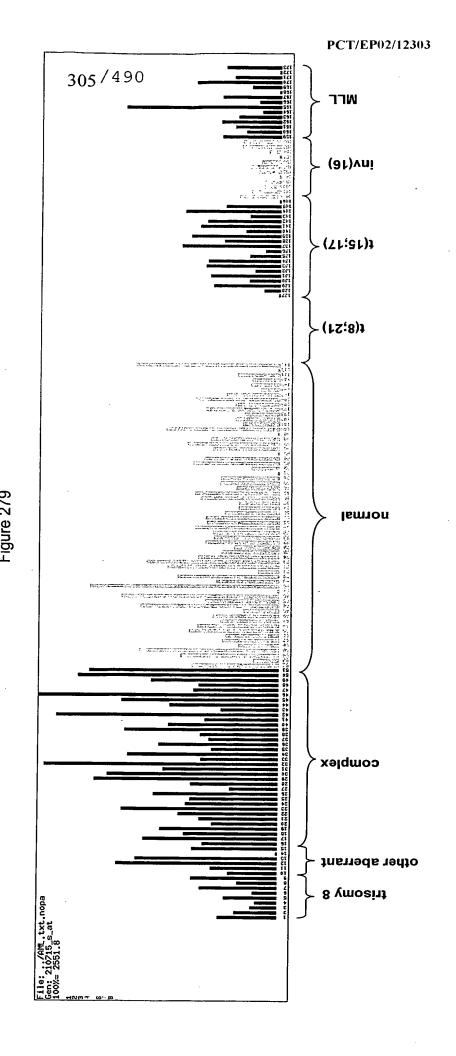
226545\_at, trisomy 8 vs. complex



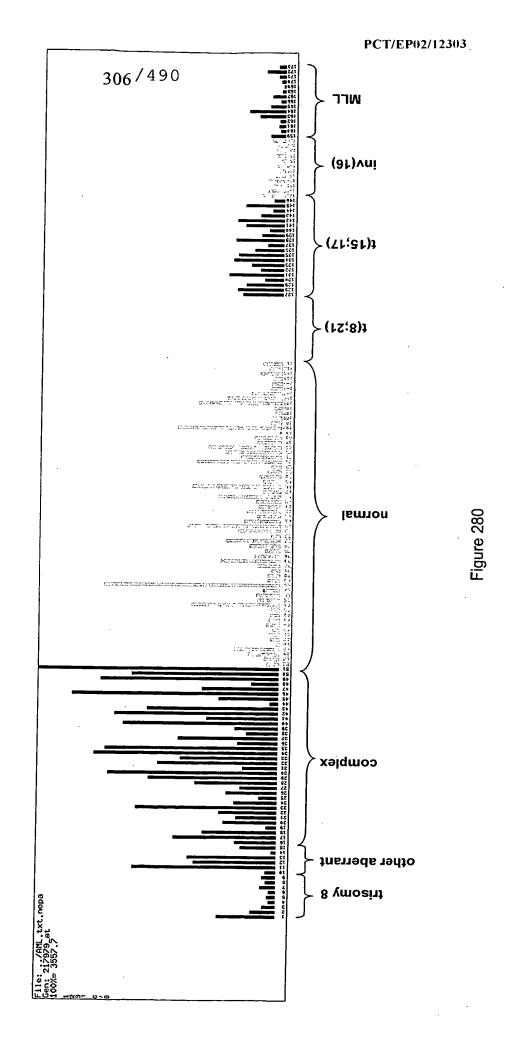
other aberrant

8 ymosint

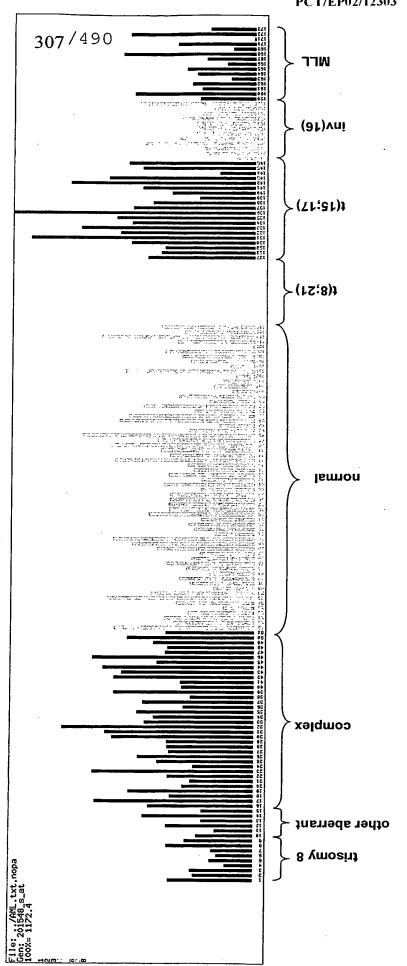
210715\_s\_at, SPINT2, trisomy 8 vs. complex



217979\_at, NET-6, trisomy 8 vs. complex

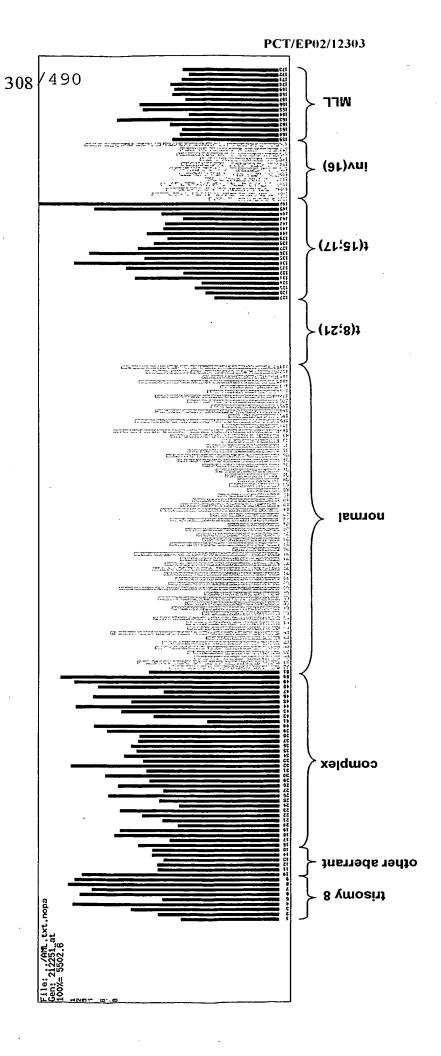


201548\_s\_at, PLU-1, trisomy 8 vs. complex

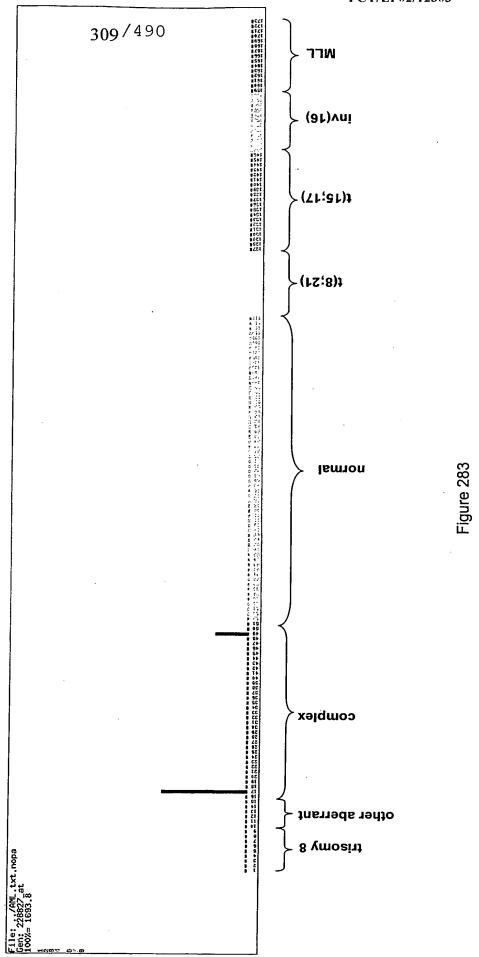


212251\_at, trisomy 8 vs. normal

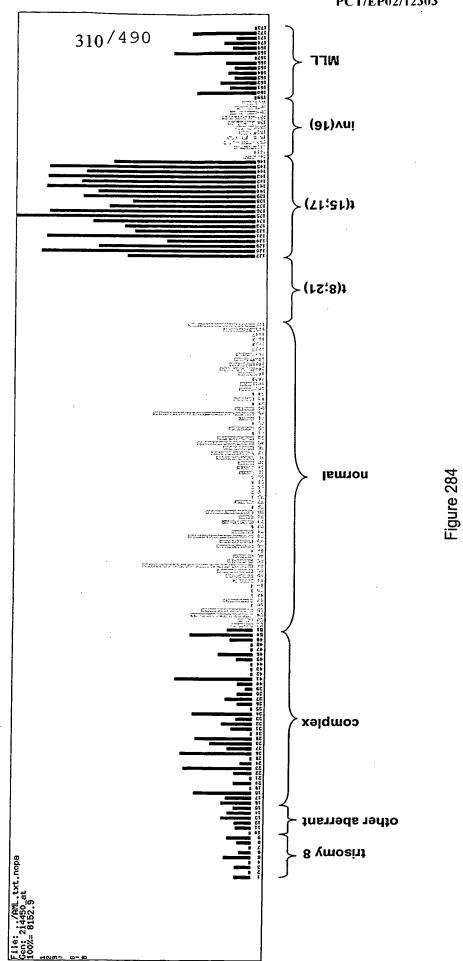
Figure 282



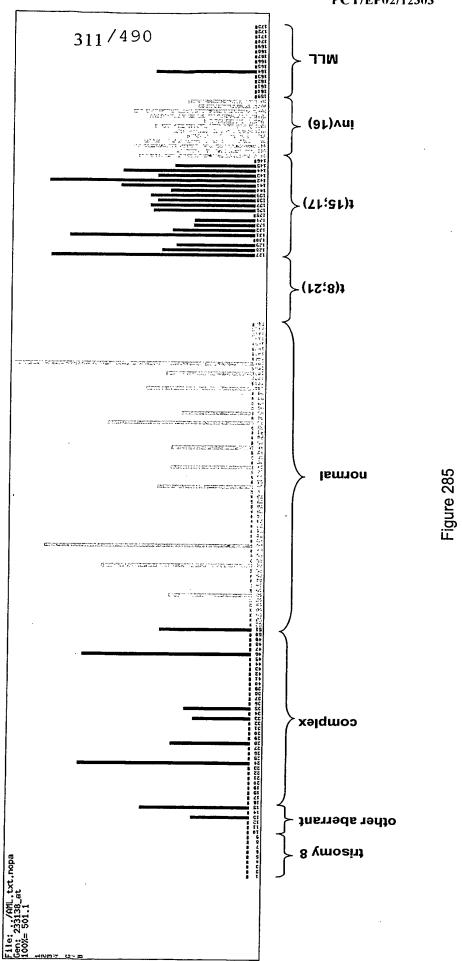
228827\_at, trisomy 8 vs. t(8;21)



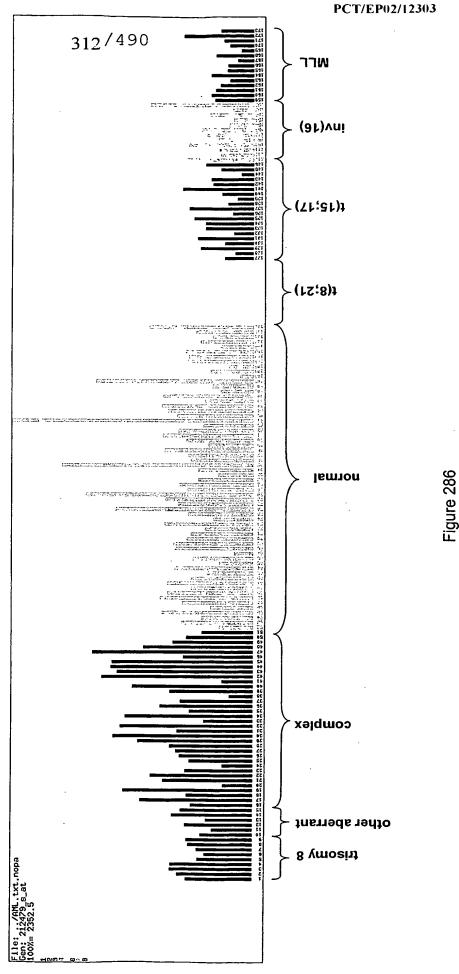
214450\_at, CTSW, trisomy 8 vs. t(15;17)



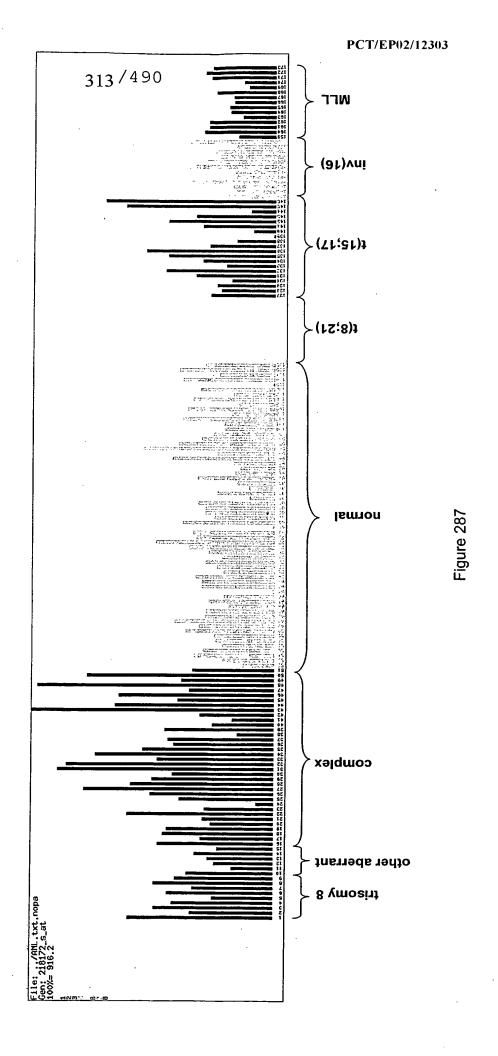
233138\_at, trisomy 8 vs. inv(16)



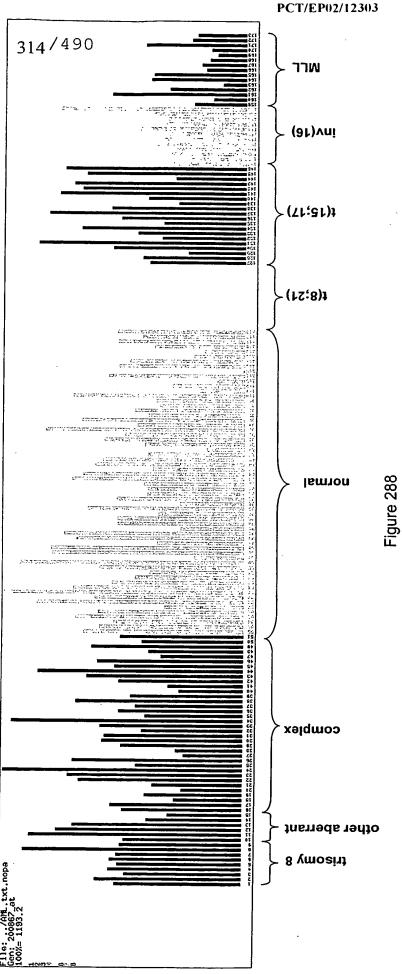
212479\_s\_at, FLJ13910, trisomy 8 vs. ML



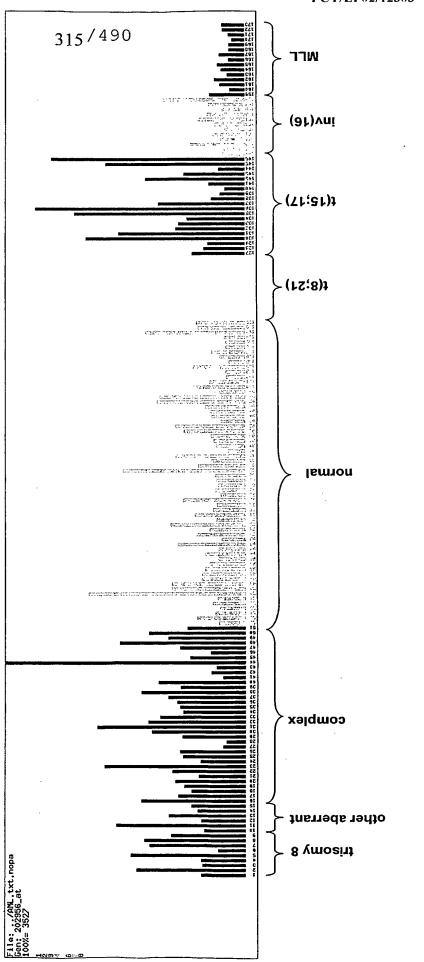
218172\_s\_at, PRO2577, trisomy 8 vs. ML



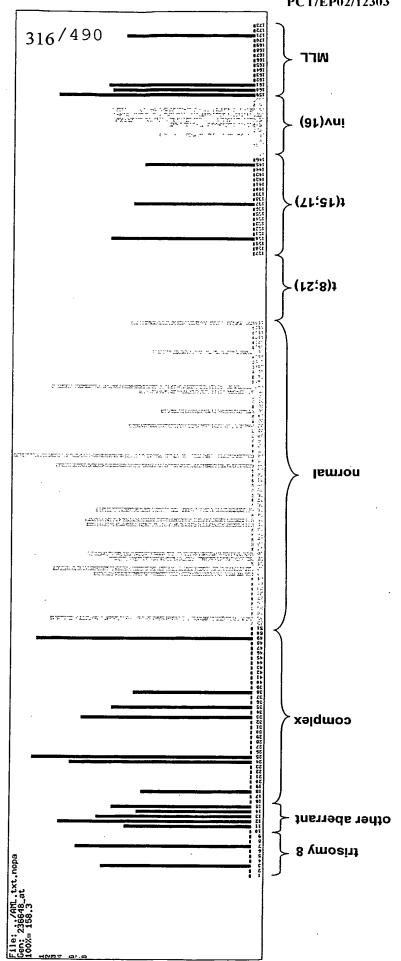
200867\_at, trisomy 8 vs. ML



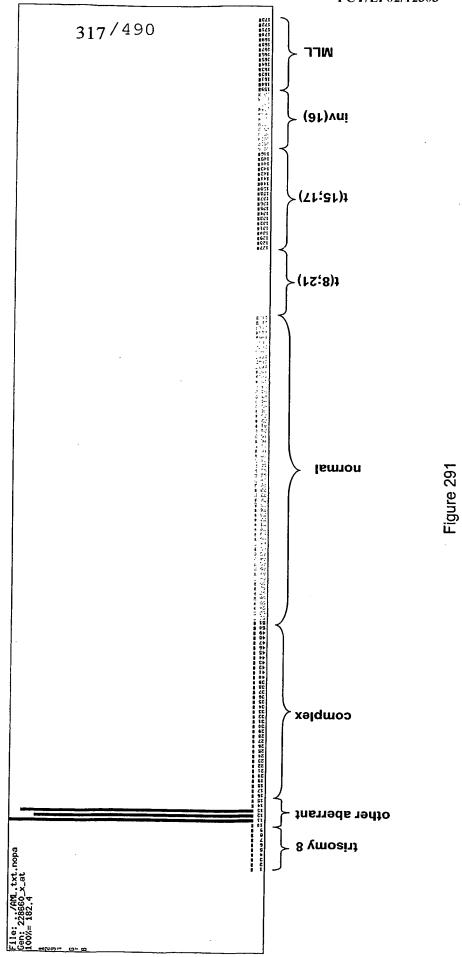
202956\_at, BIG1, trisomy 8 vs. MLL



236648\_at, other aberrant vs. all other AM

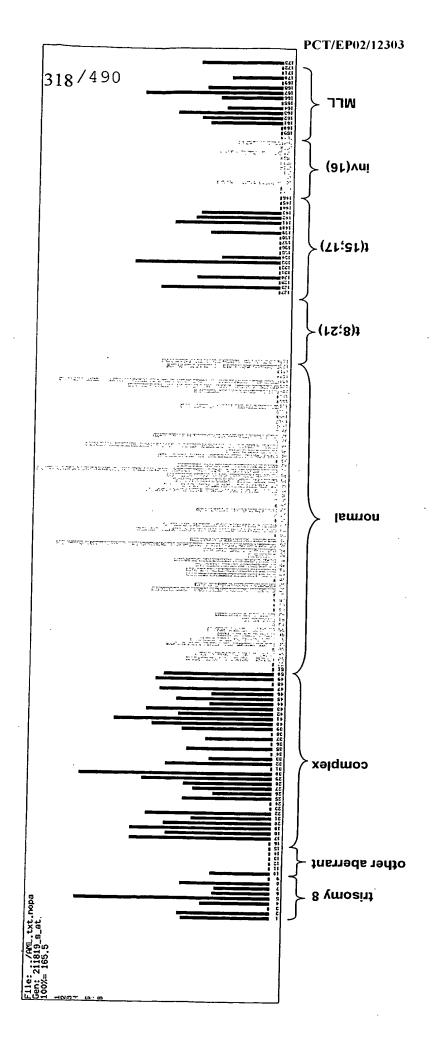


228660\_x\_at, SEMA4F, other aberrant vs. all other AML

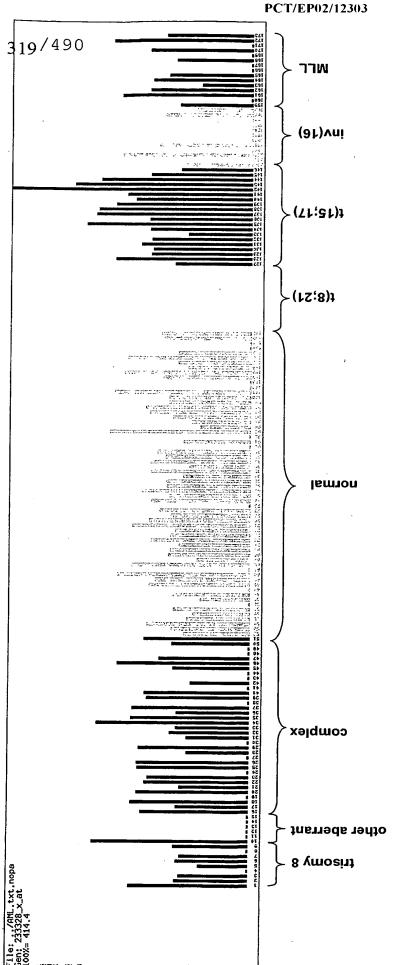


211819\_s\_at, SH3D5, other aberrant vs. complex

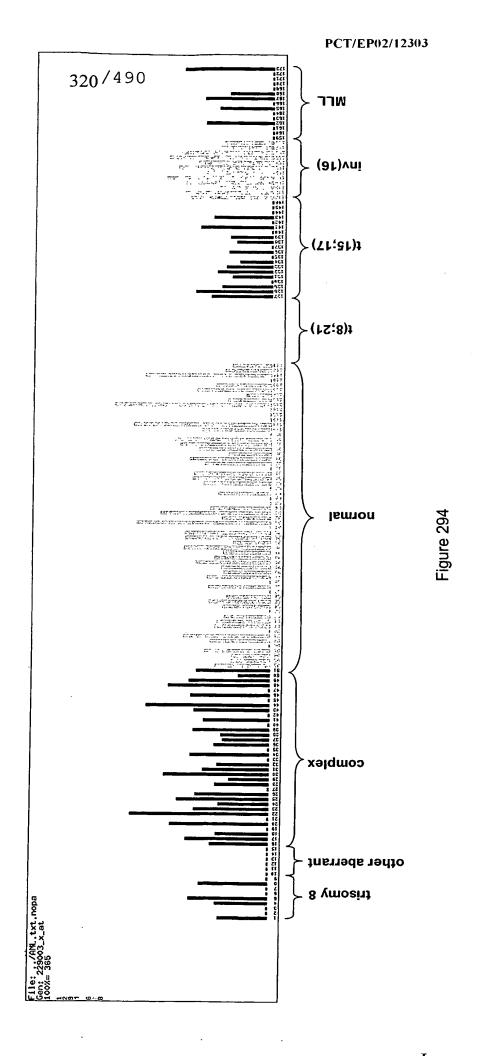




### 233328\_x\_at, other aberrant vs. complex

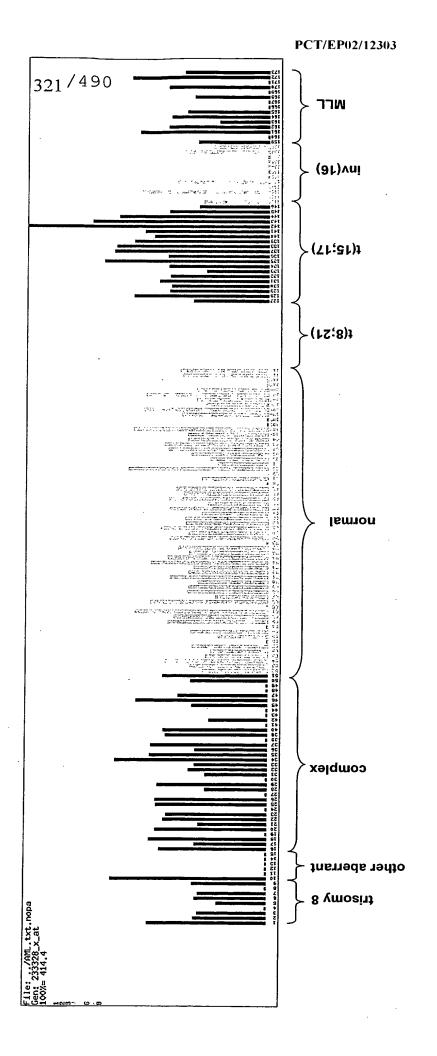


229003\_x\_at, other aberrant vs. complex



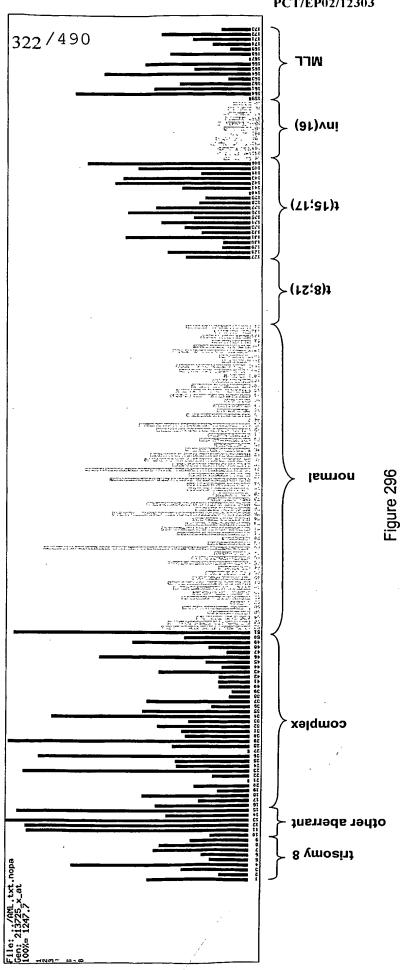
### 233328\_x\_at, other aberrant vs. normal

Figure 295



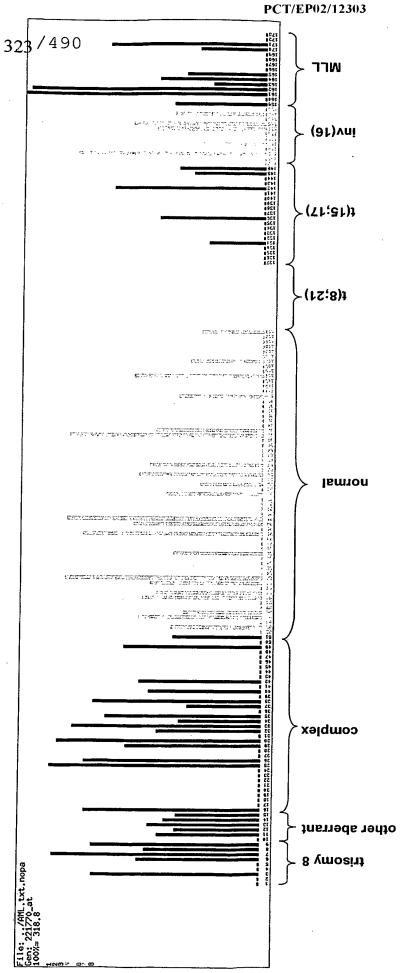
PCT/EP02/12303

213725\_x\_at, other aberrant vs. normal

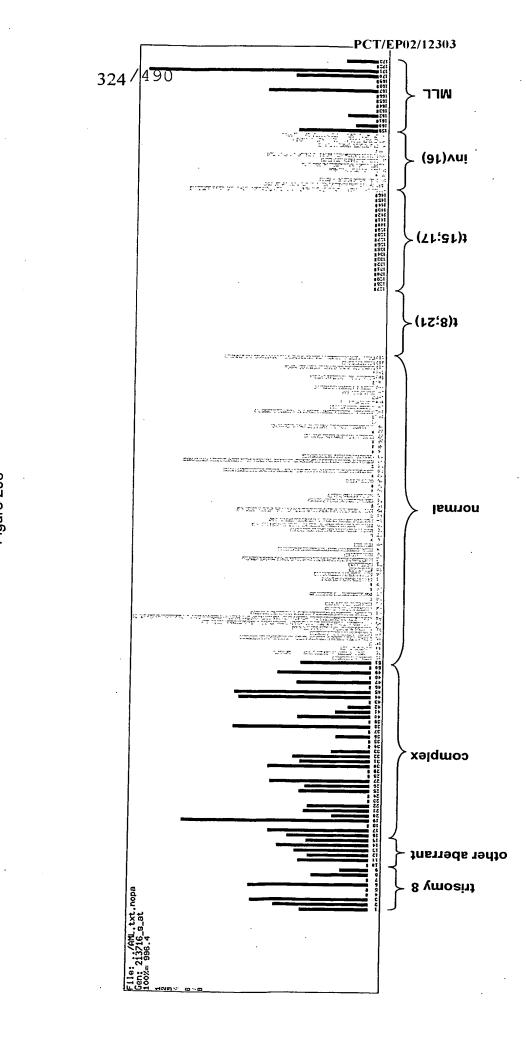


221770\_at, RPE, other aberrant vs. t(8;21)



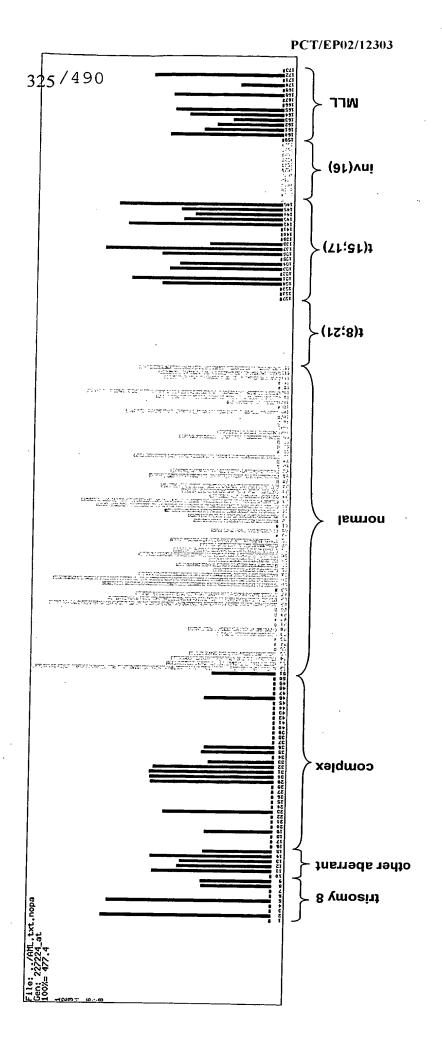


# 213716\_s\_at, SECTM1, other aberrant vs. t(15;17)

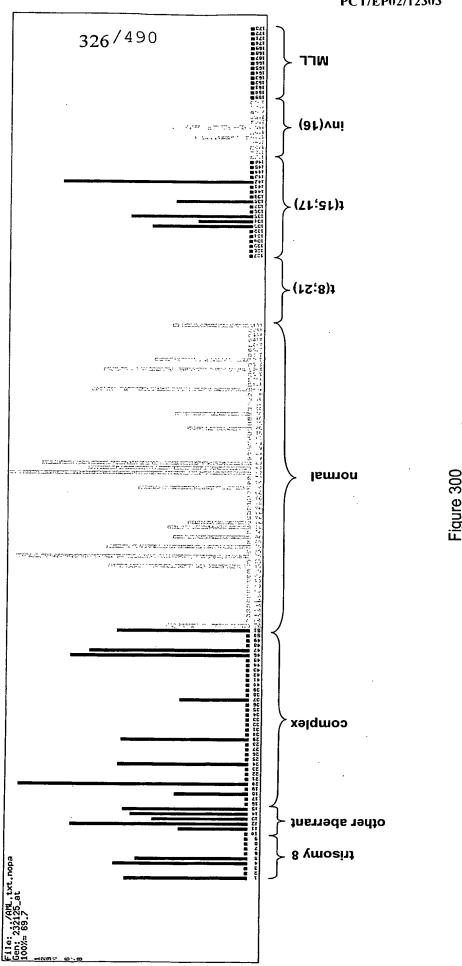


#### 227224\_at, other aberrant vs. inv(16)

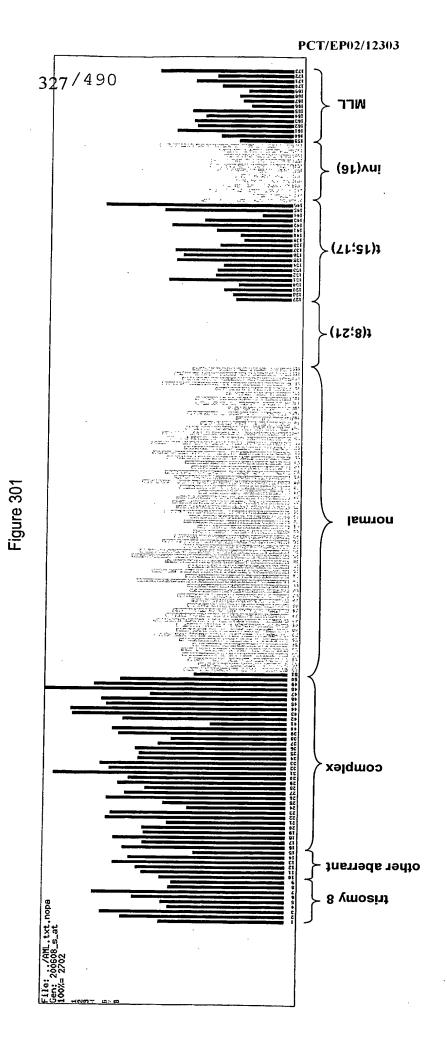
Figure 299



232125\_at, other aberrant vs. MLI

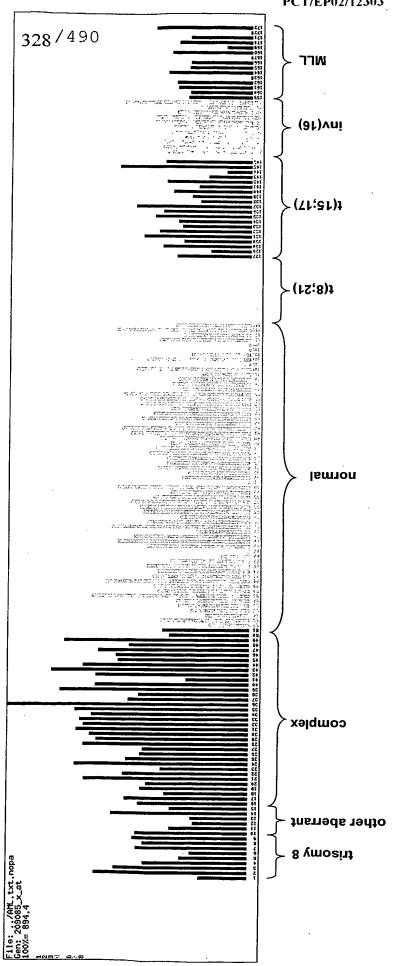


200608\_s\_at, RAD21, complex vs. all other AMI



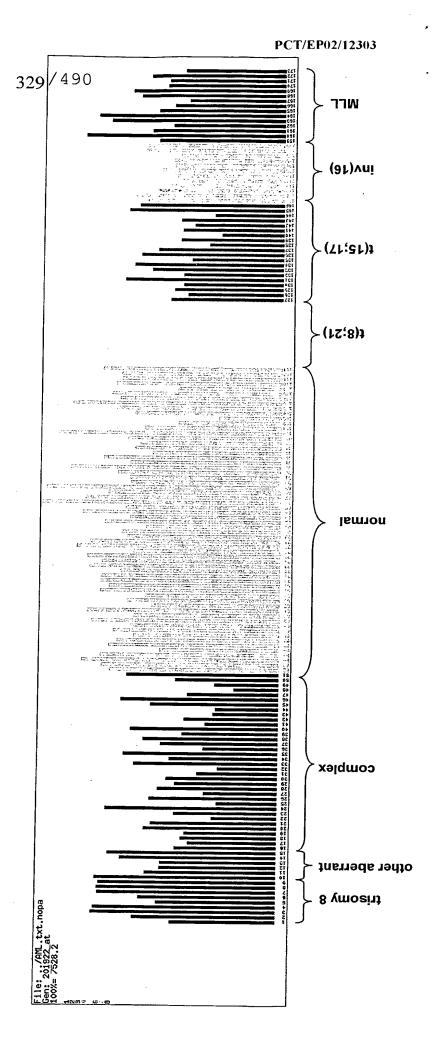
## 209085\_x\_at, RFC1, complex vs. all other AMI

Figure 302

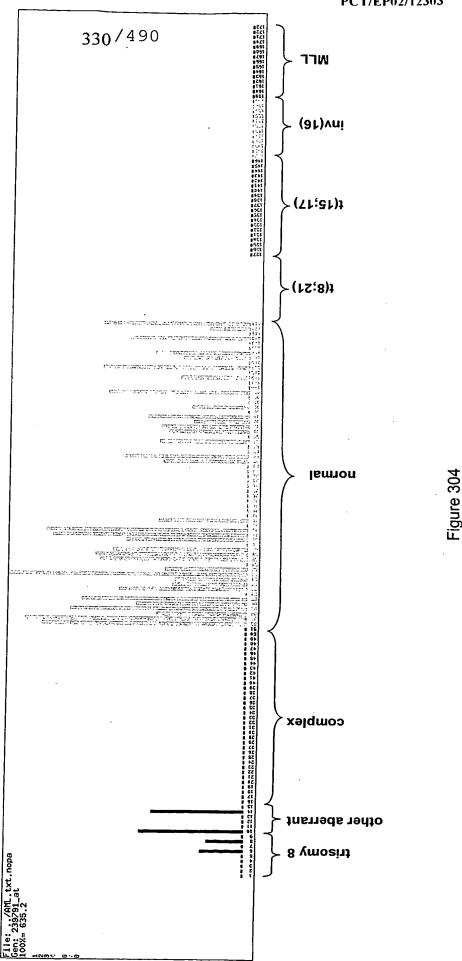


### 201922\_at, YR-29, complex vs. normal

Figure 303

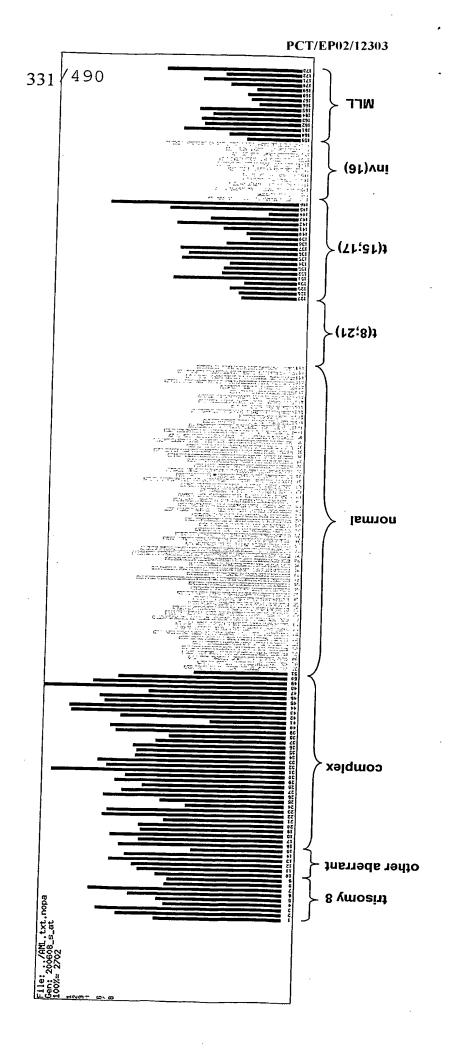


### 239791\_at, HOXB6, complex vs. norma

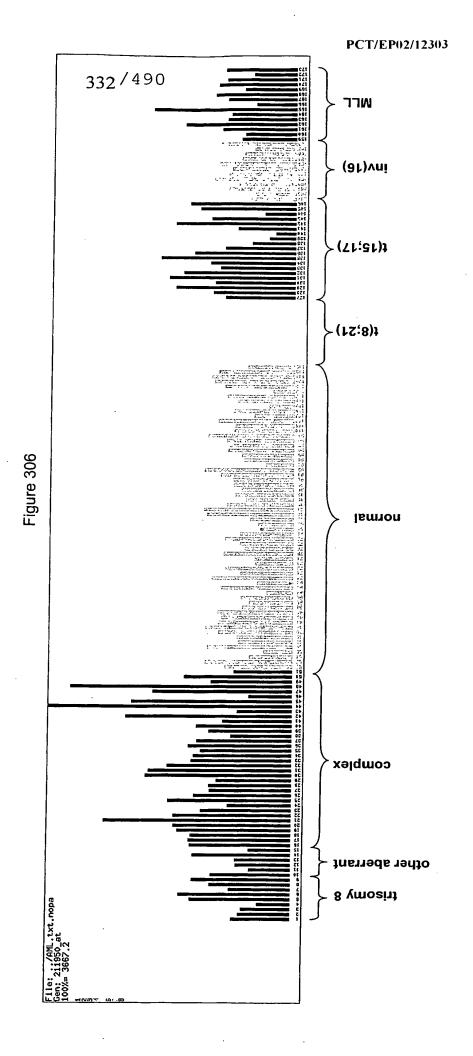


200608\_s\_at, RAD21, complex vs. normal

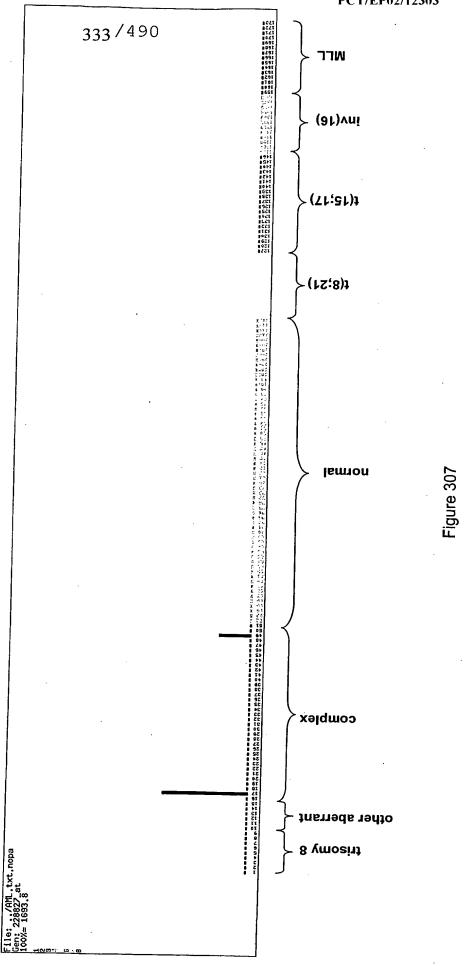
Figure 305



211950\_at, RBAF600, complex vs. normal



228827\_at, complex vs. t(8;21)

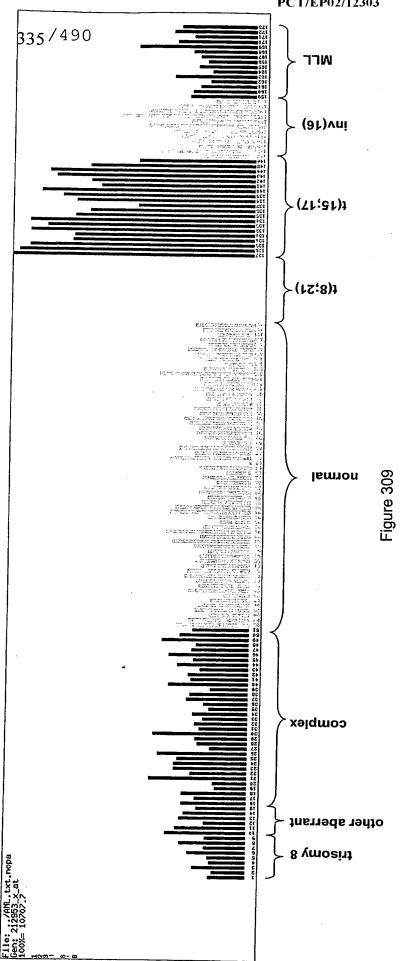


204249\_s\_at, LMO2, complex vs. t(8;21

Figure 308

PCT/EP02/12303

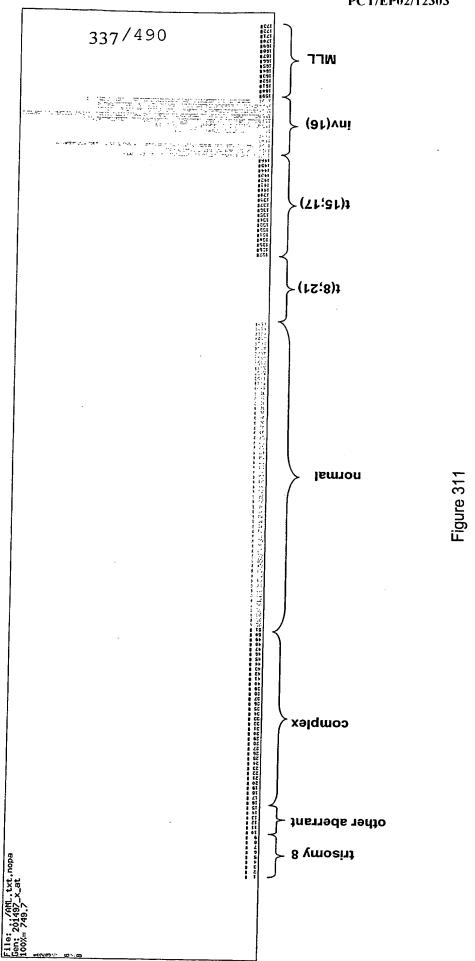
212953\_x\_at, CALR, complex vs. t(15;17)



209190\_s\_at, DIAPH1, complex vs. inv(16)

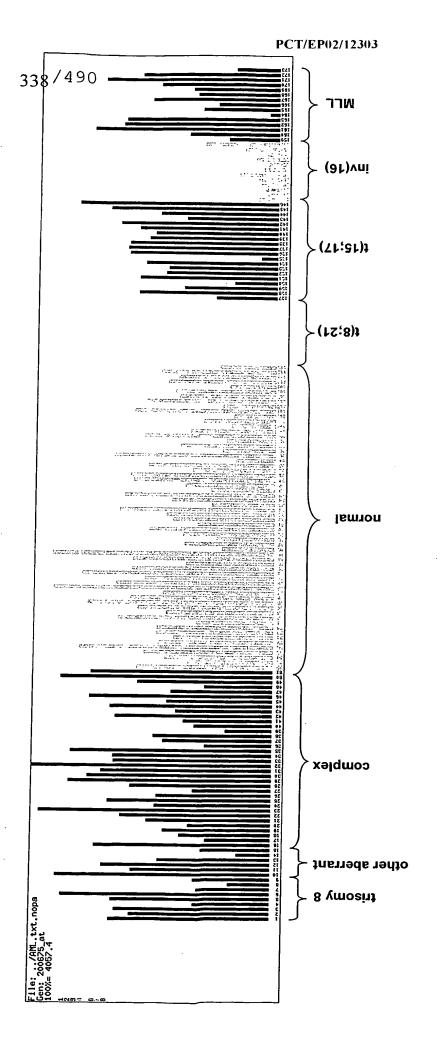
PCT/EP02/12303 336/490 MLL (at)vni - (Tr;21)3 ≻(rz;8)± Figure 310 normal complex other aberrant frisomy 8

201497\_x\_at, MYH11, complex vs. inv(16)

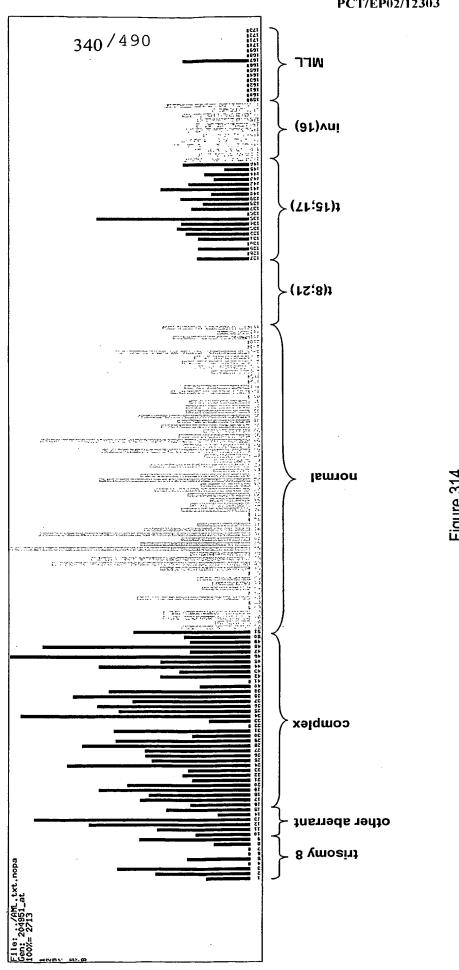


#### 200675\_at, CD81, complex vs. inv(16)

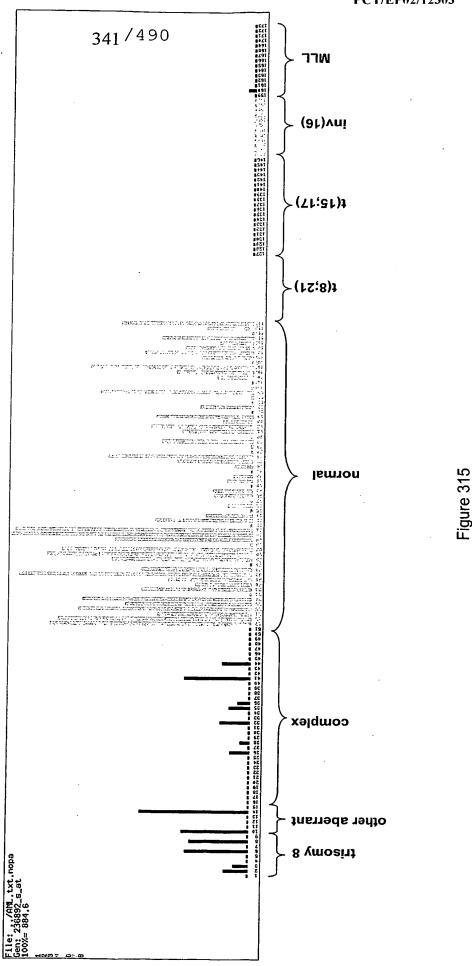
Figure 312



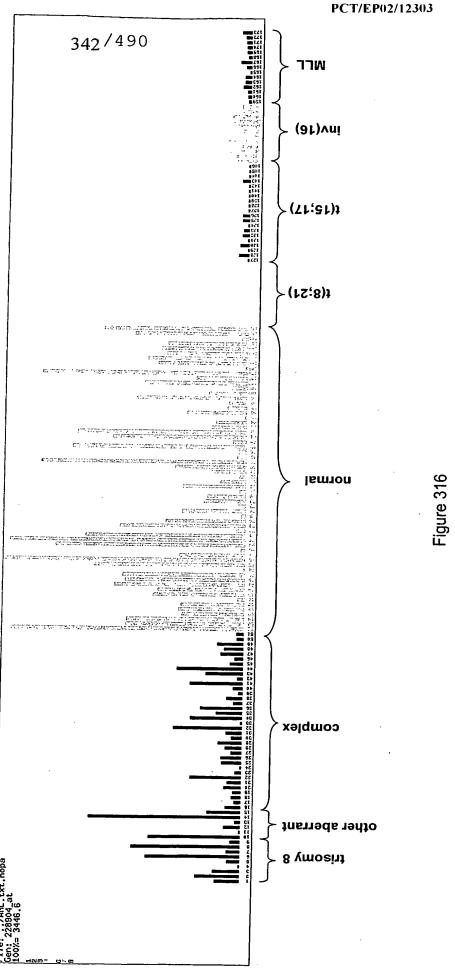
204951\_at, ARHH, complex vs. Ml



236892\_s\_at, HOXB6, normal vs. all other AMI



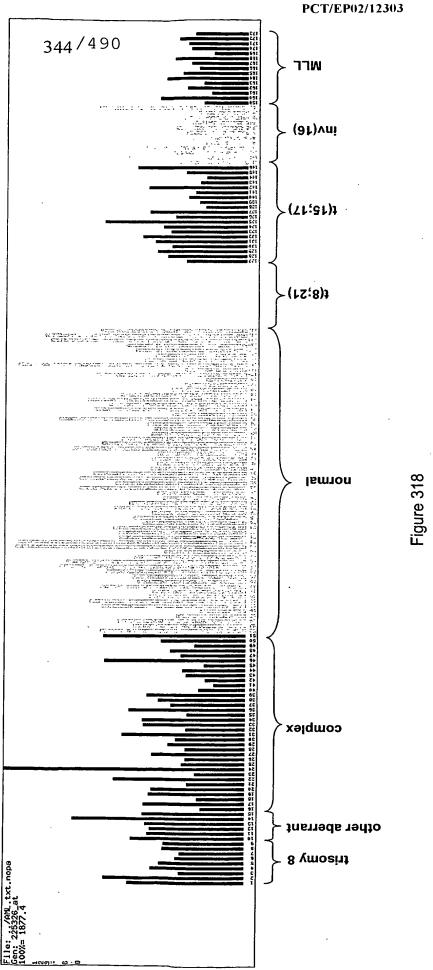
228904\_at, normal vs. all other AM



PCT/EP02/12303

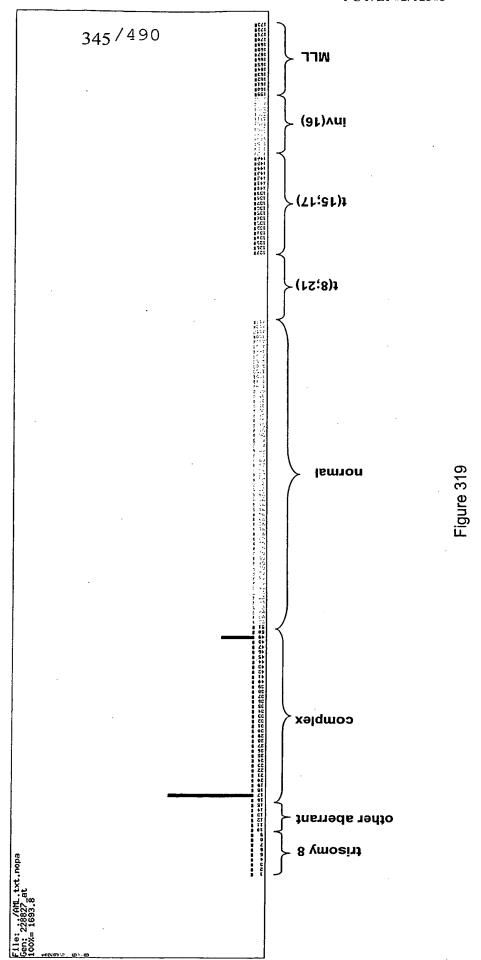
### 200679\_x\_at, HMG1, normal vs. all other AML

225326\_at, KIAA1311, normal vs. all other AMI

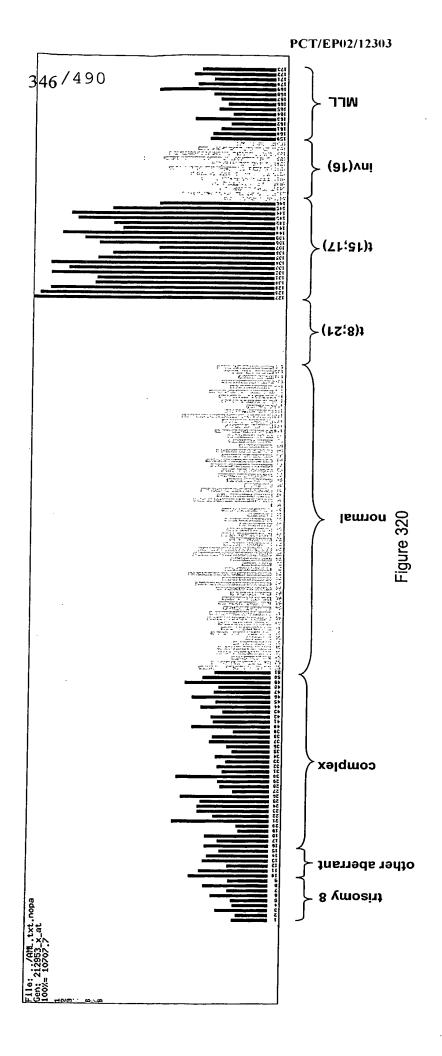


BNSDOCID: <WO\_\_\_\_03039443A2\_I\_>

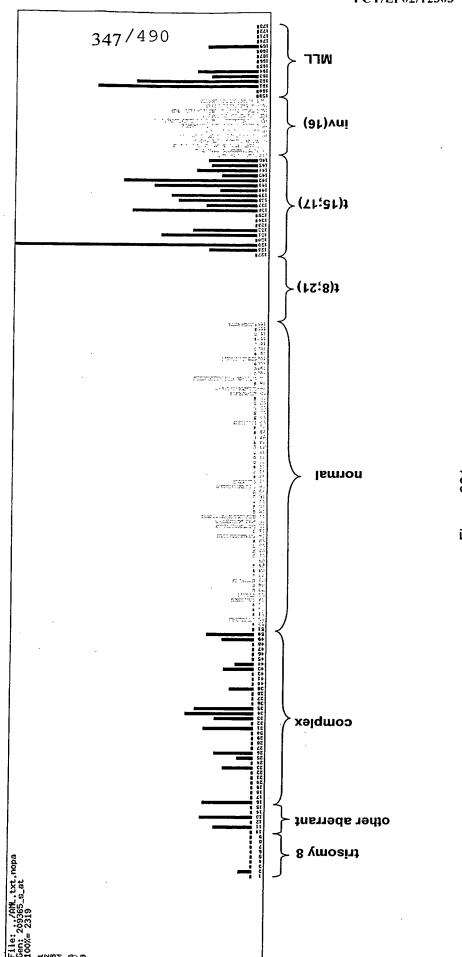
228827\_at, normal vs. t(8;21)



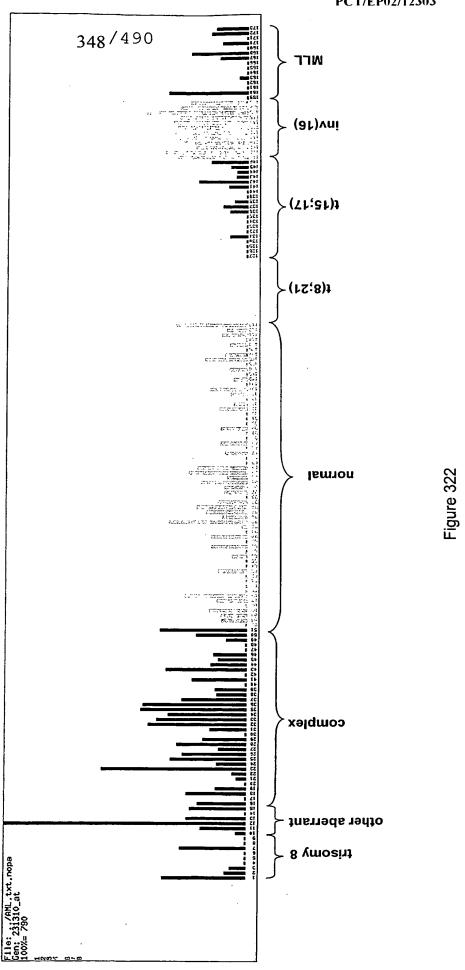
212953\_x\_at, CALR, normal vs. t(15;17)



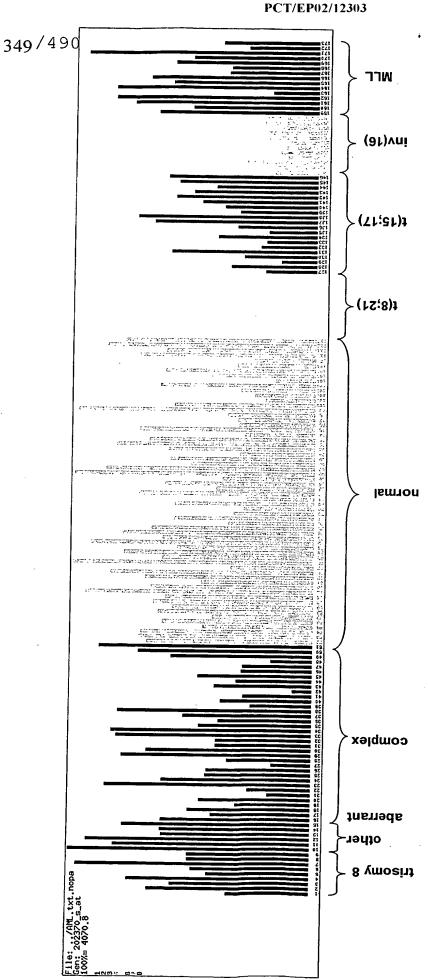
209365\_s\_at, ECM1, normal vs. inv(16)



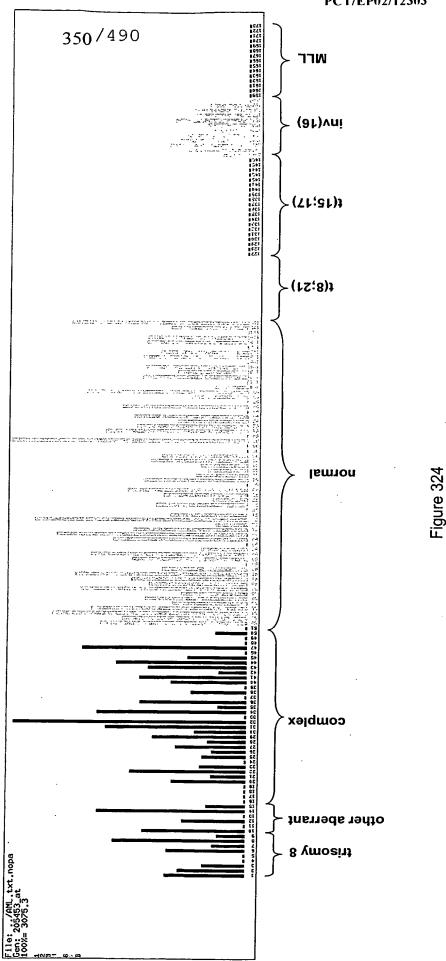
231310\_at, normal vs. inv(16)



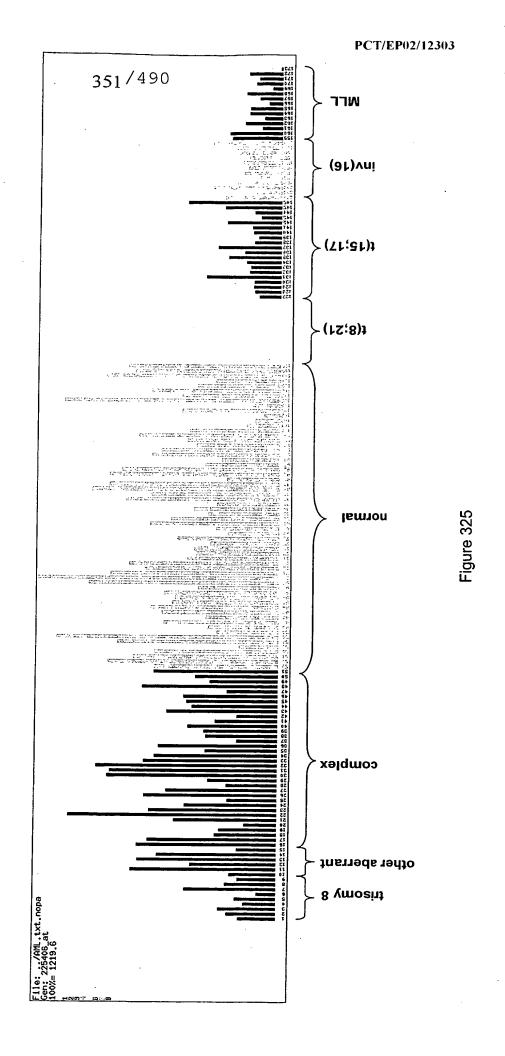
202370\_s\_at, CBFB, normal vs. inv(16)



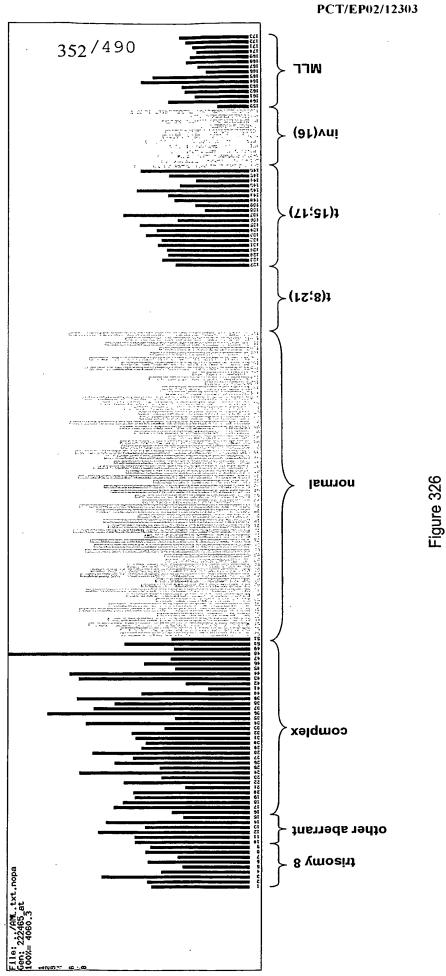
205453\_at, HOXB2, normal vs. MLL



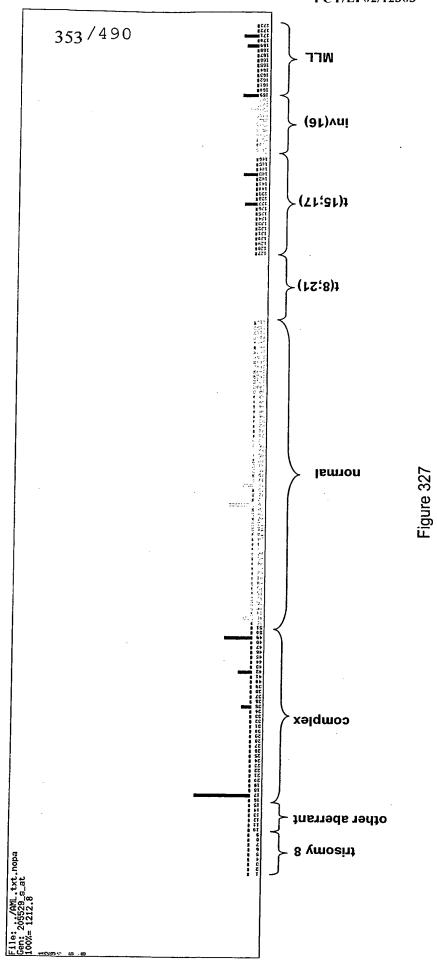
225406\_at, TSG, normal vs. MLL



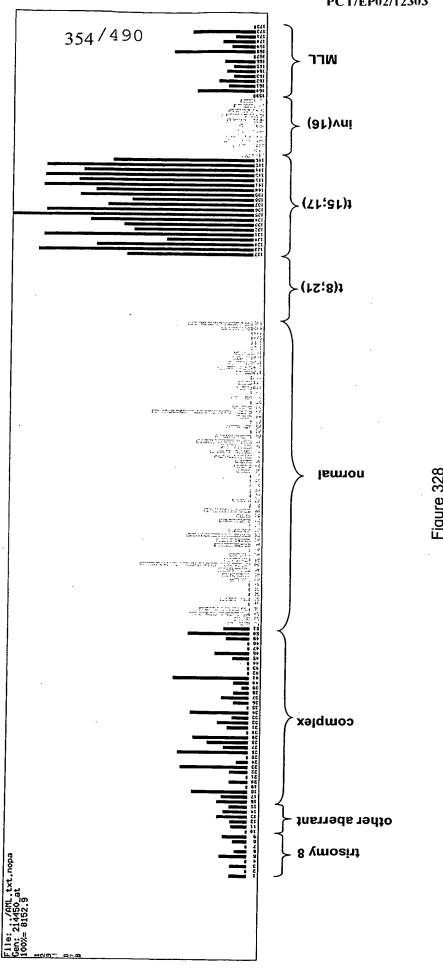
222464\_at, C15orf15, normal vs. ML



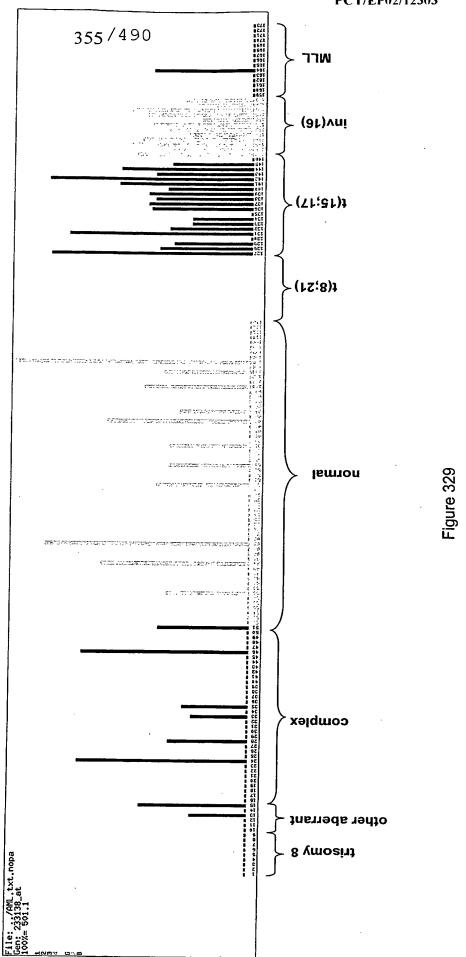
205529\_s\_at, CBFA2T1, t(8;21) vs. all other AMI



214450\_at, CTSW, t(8;21) vs. t(15;17)

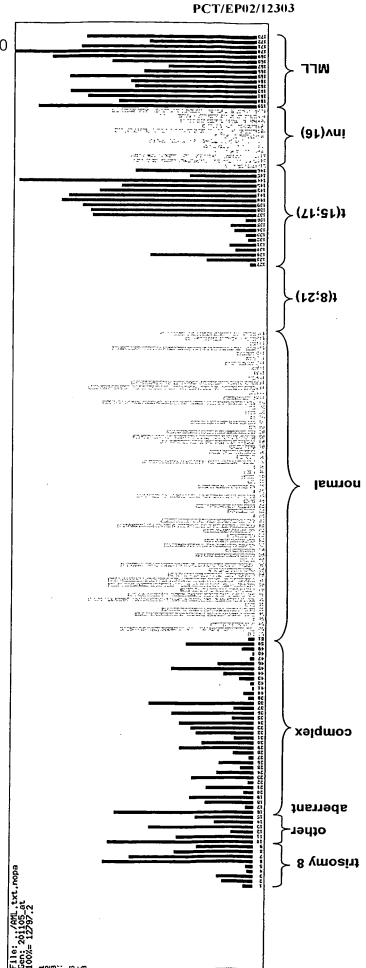


233138\_at, t(8;21) vs. inv(16)

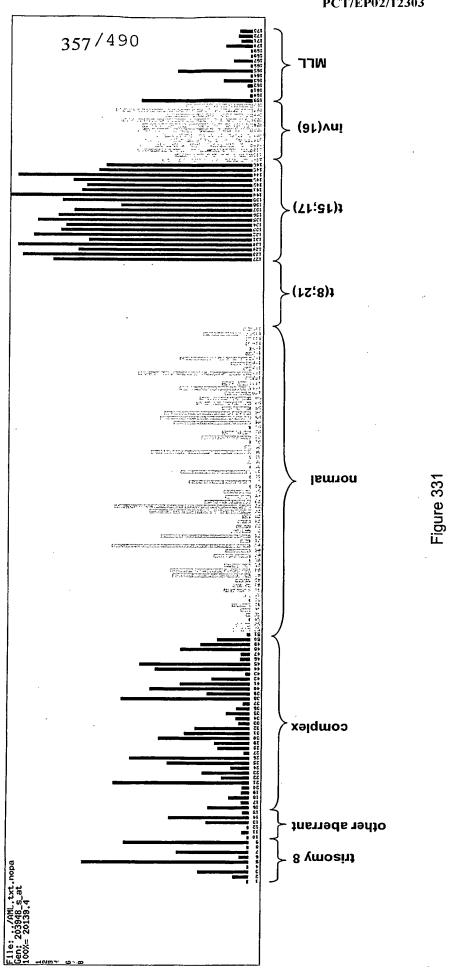


201105\_at, LGALS1, t(8;21) vs. ML

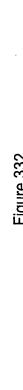


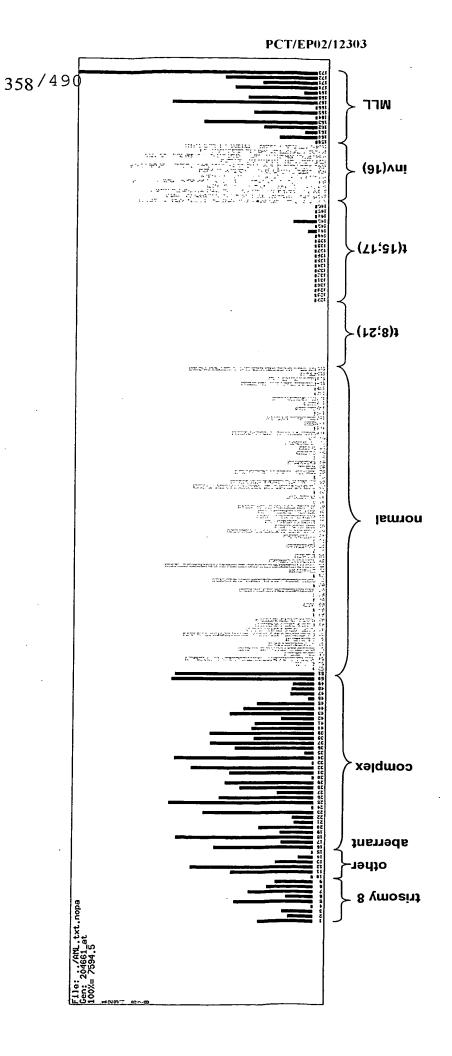


203948\_s\_at, MPO, t(15;17) vs. all other AMI

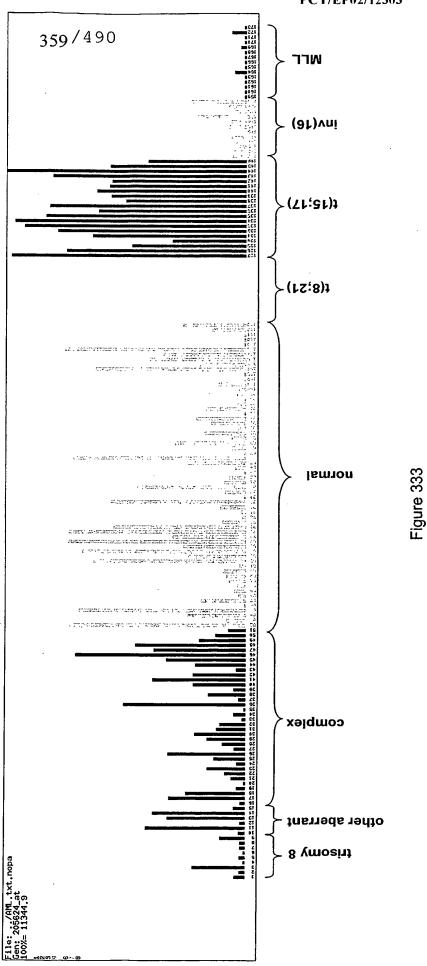


204661\_at, CDW52, t(15;17) vs. inv(16)

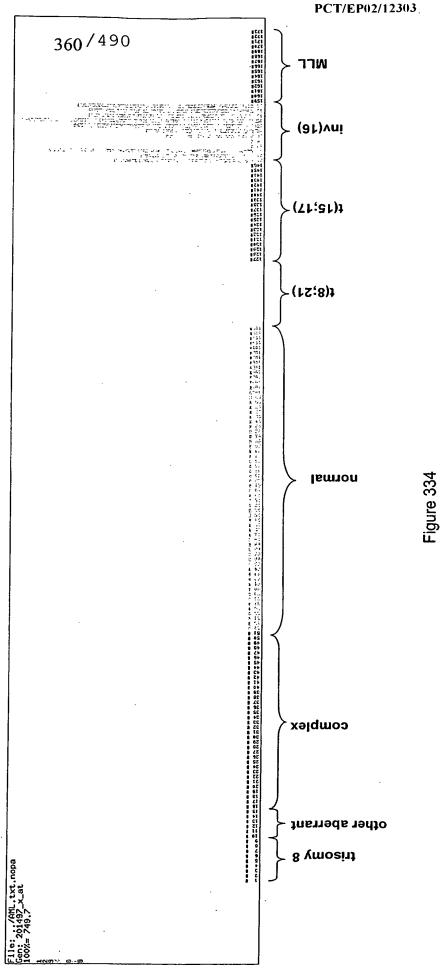




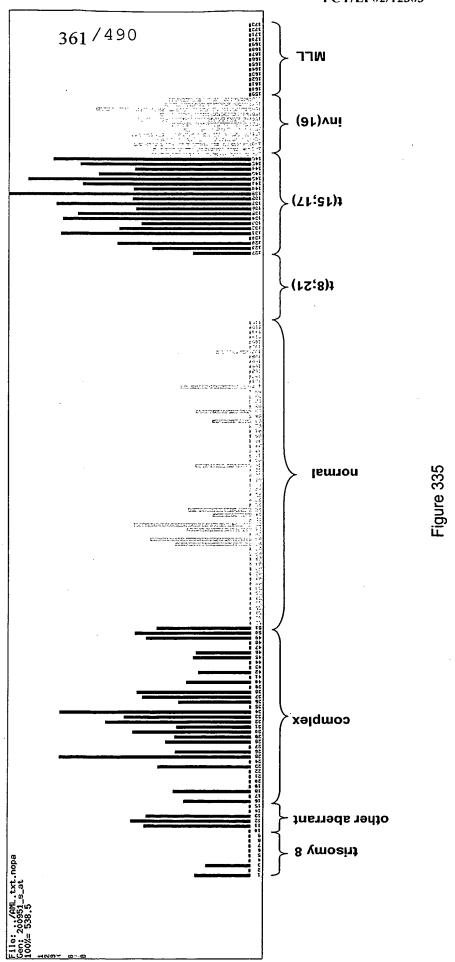
205624\_at, CPA3, t(15;17) vs. MLL



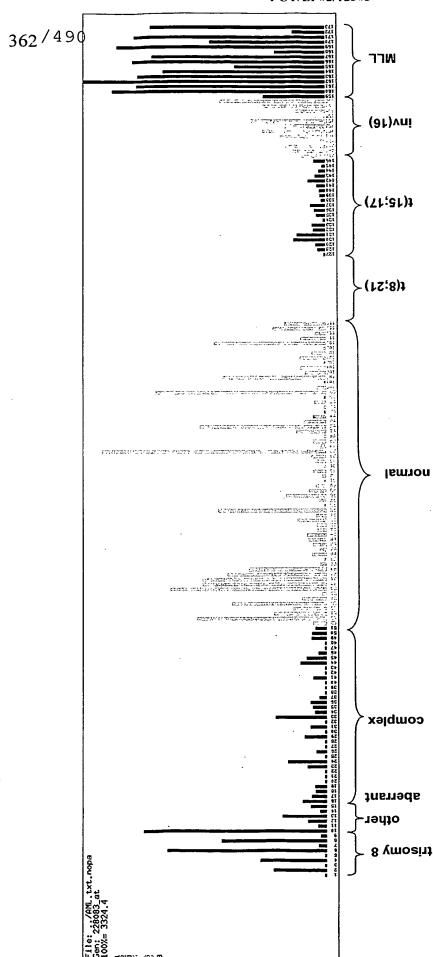
201497\_x\_at, MYH11, inv(16) vs. all other AMI



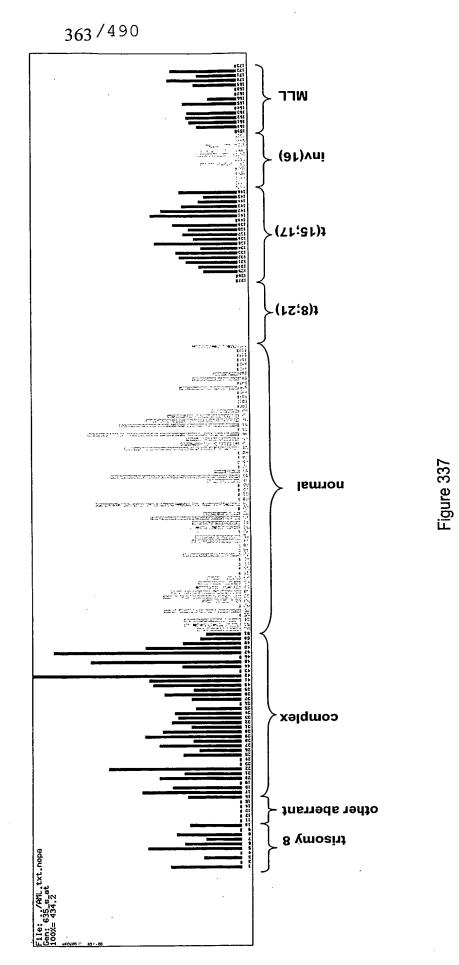
200951\_s\_at, CCND2, inv(16) vs. MLI







635\_s\_at, PPP2R5B, other low



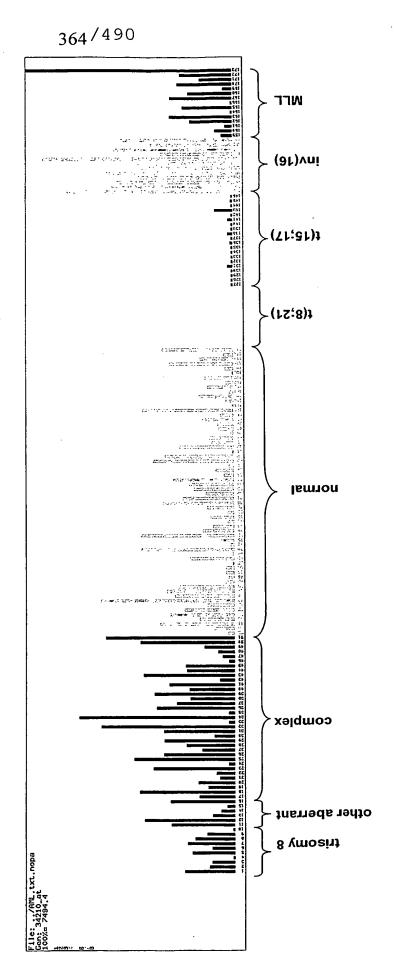
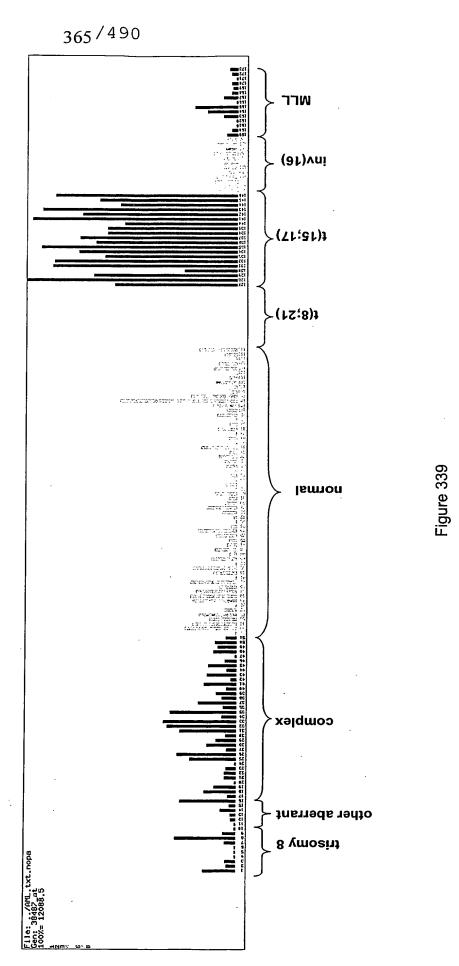
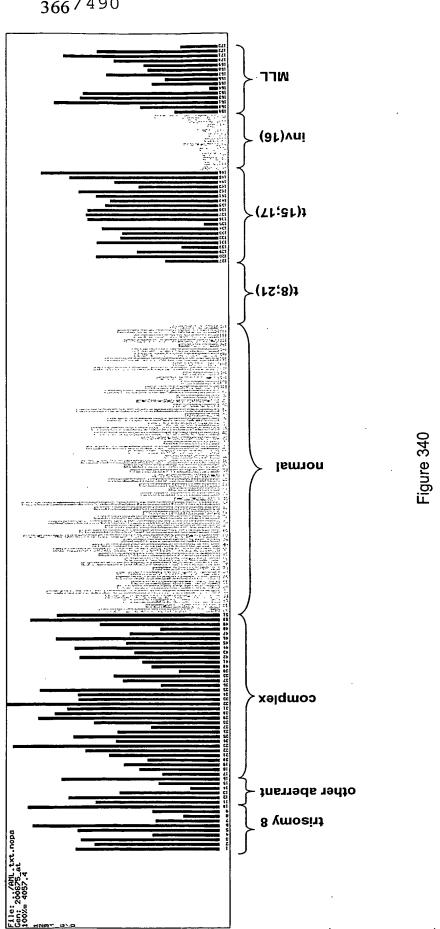


Figure 33

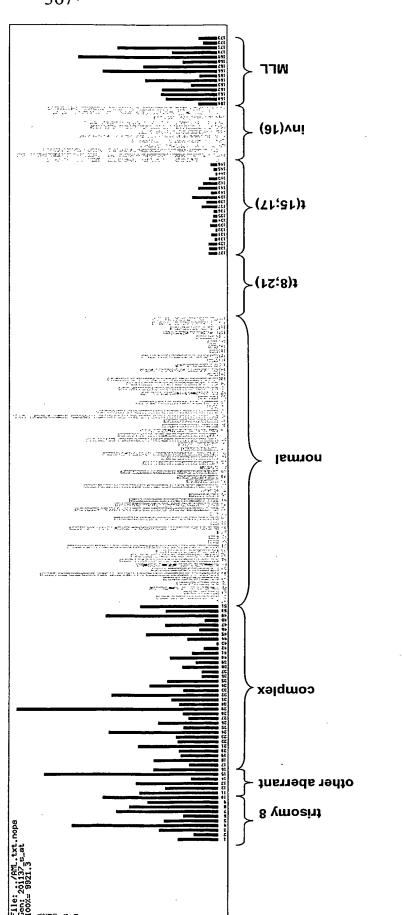


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200675\_at, CD81, AML inv(16) low

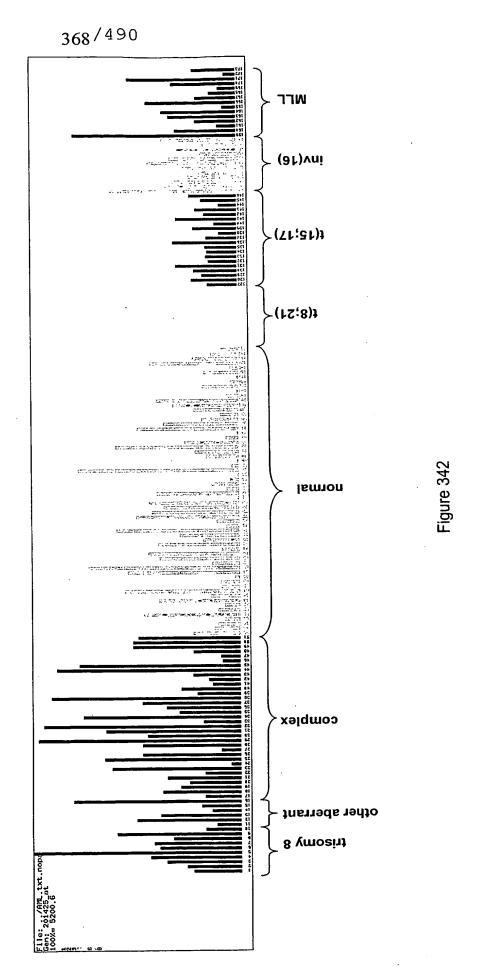


201137\_s\_at, HLA-DPB1, AML t(15;17) low



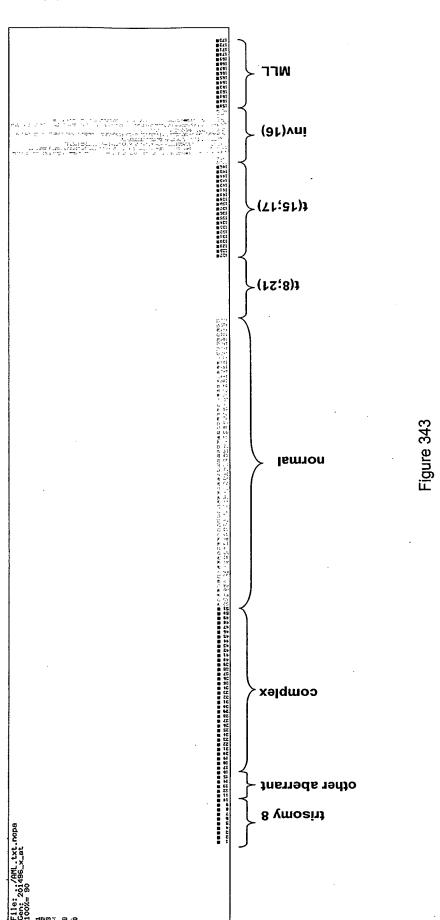
BNSDOCID: <WO\_\_\_\_\_03039443A2\_I\_>

201425\_at, ALDH2, AML t(8;21) low

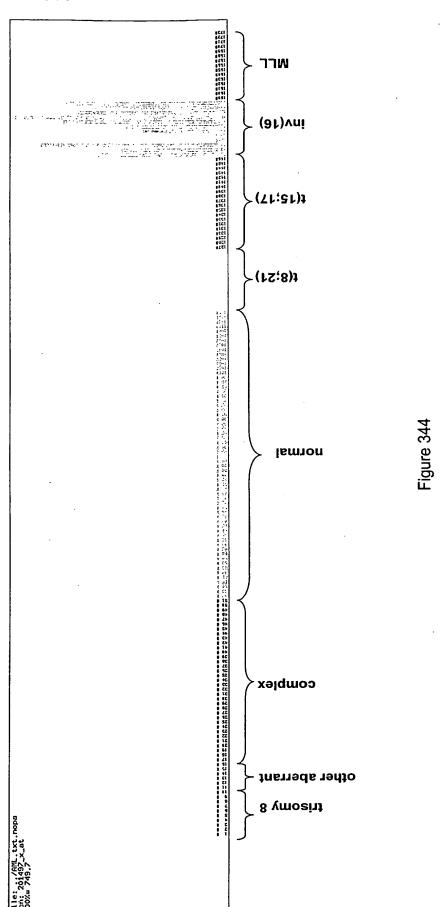


BNSDOCID: <WO\_\_\_\_03039443A2\_I\_>

201496\_x\_at, MYH11, AML inv(16) high

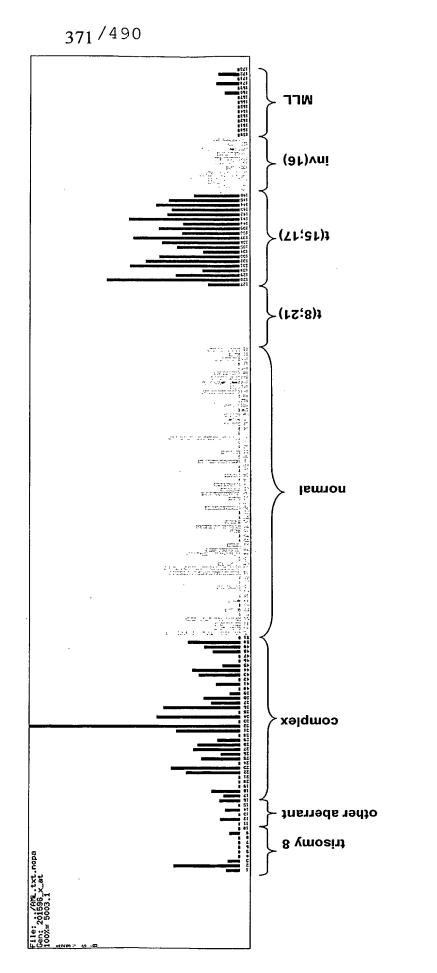


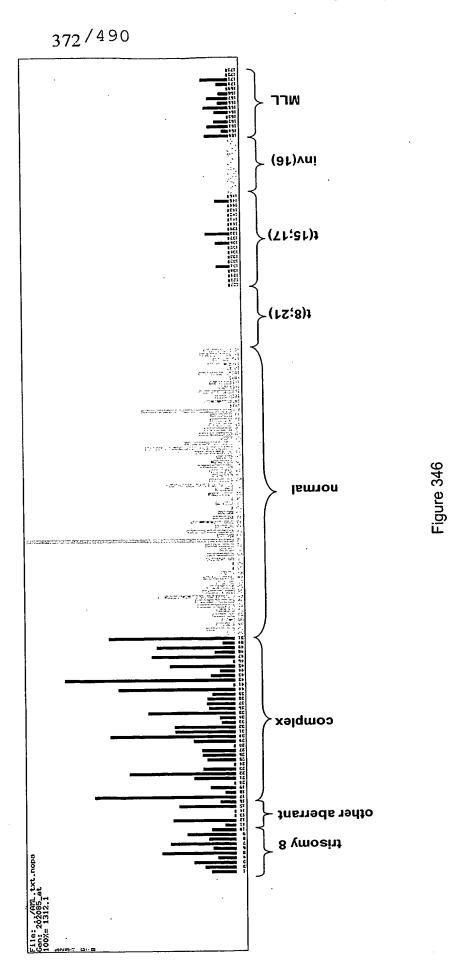
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201497\_x\_at, MYH11, AML inv(16) high

201596\_x\_at, KRT18, AML t(8;21) low



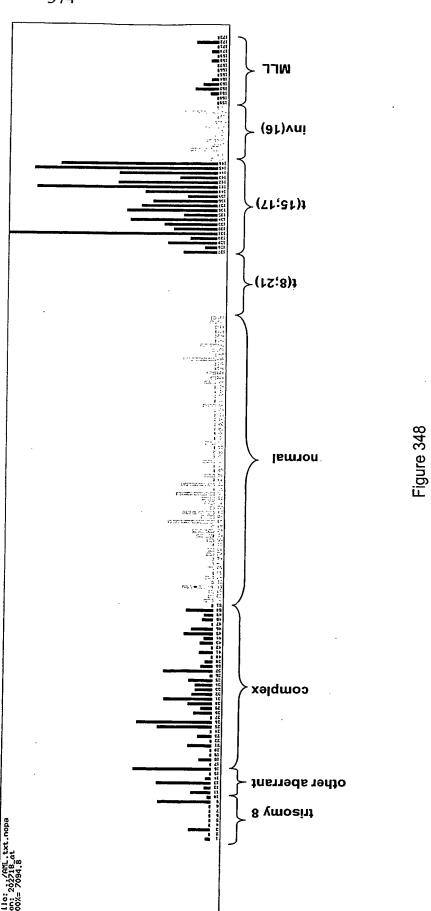


373/490

WLL (at)vni 202619\_s\_at, PLOD2, AML MLL low (42:41) (12;8)1 normal complex other aberrant trisomy 8

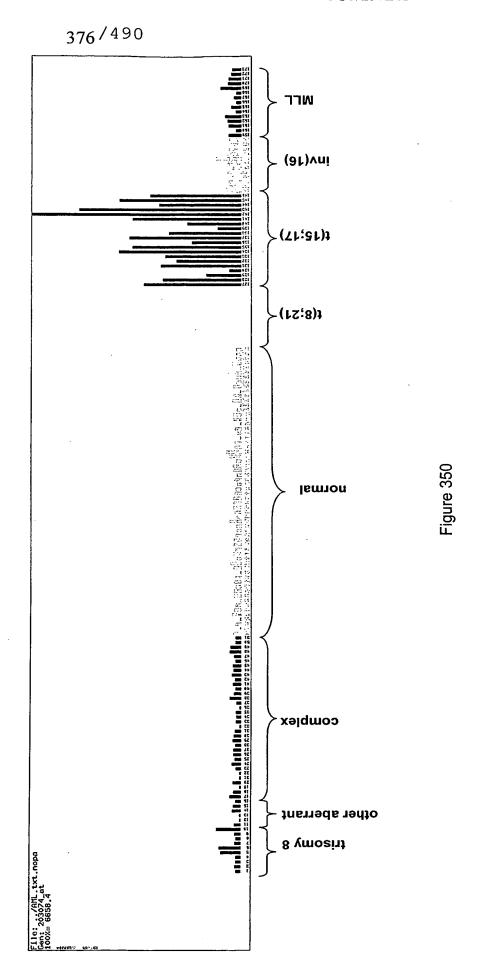
igure 347

202718\_at, IGFBP2, AML t(15;17) high

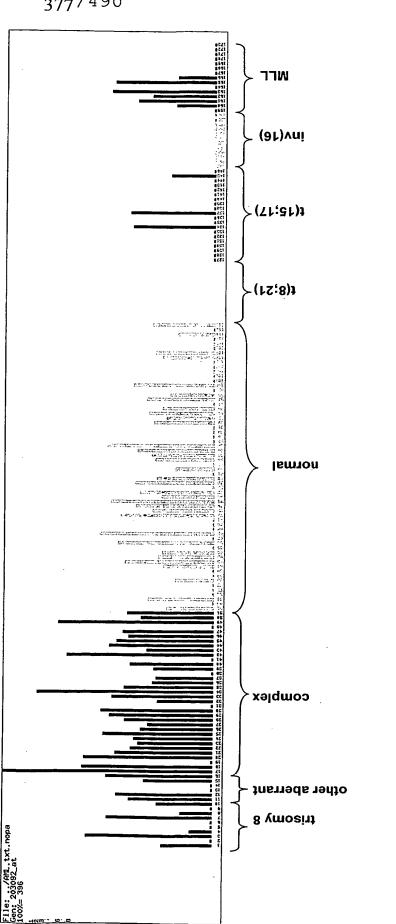


igure 349

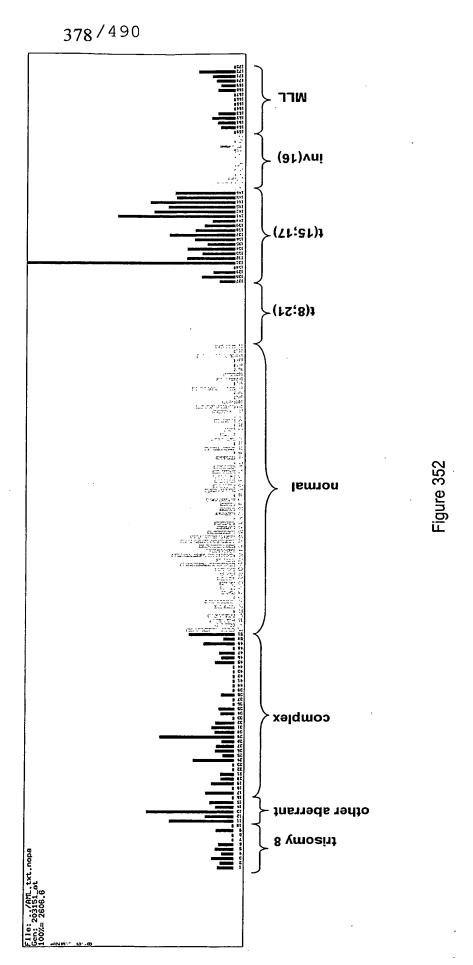
203074\_at, ANXA8, AML t(15;17) high



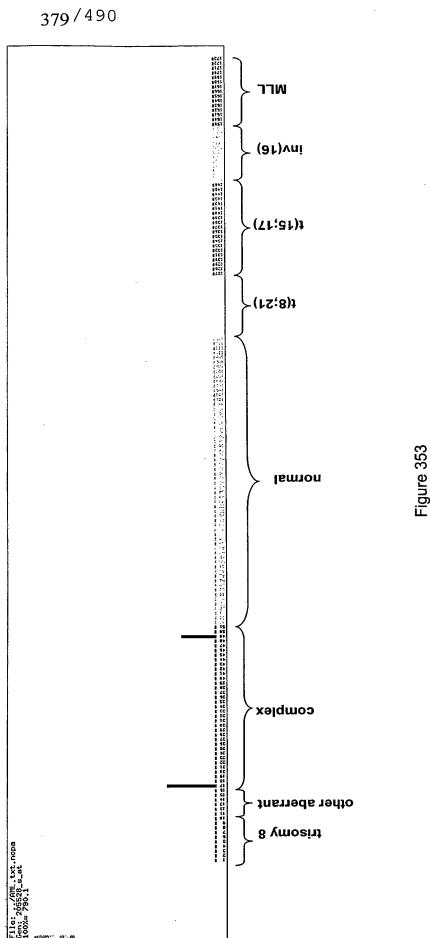
203092\_at, TIMM44, AML inv(16) low



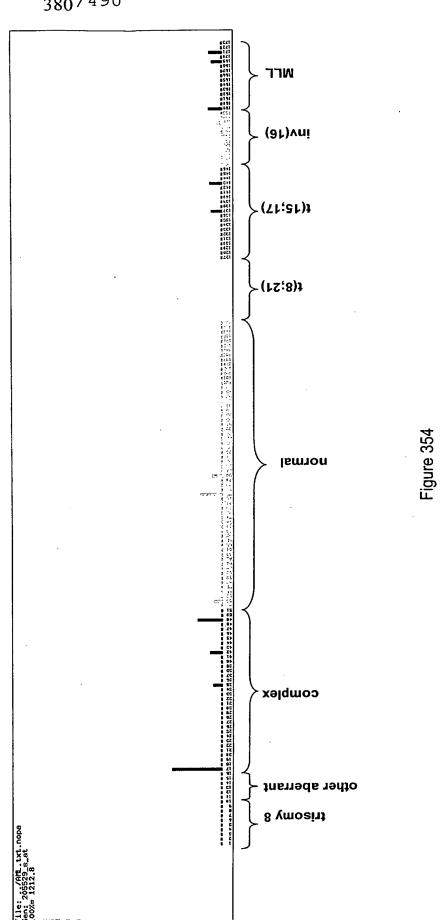
203151\_at, MAP1A, AML t(8;21) low



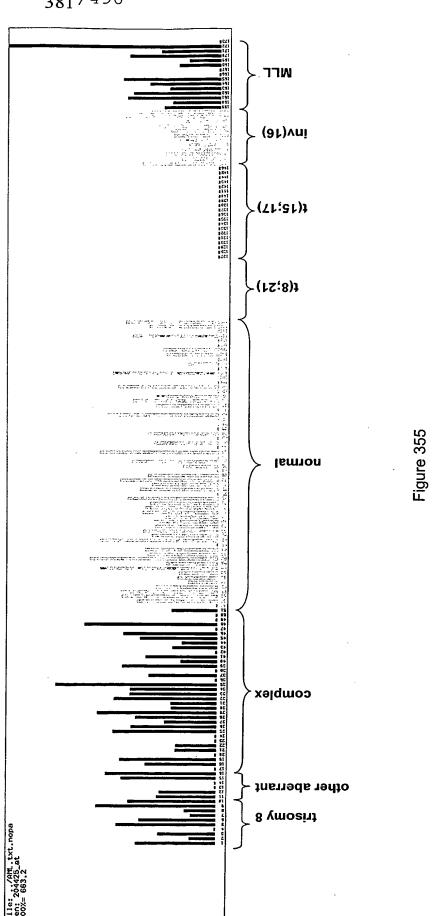
205528\_s\_at, CBFA2T1, AML t(8;21) high



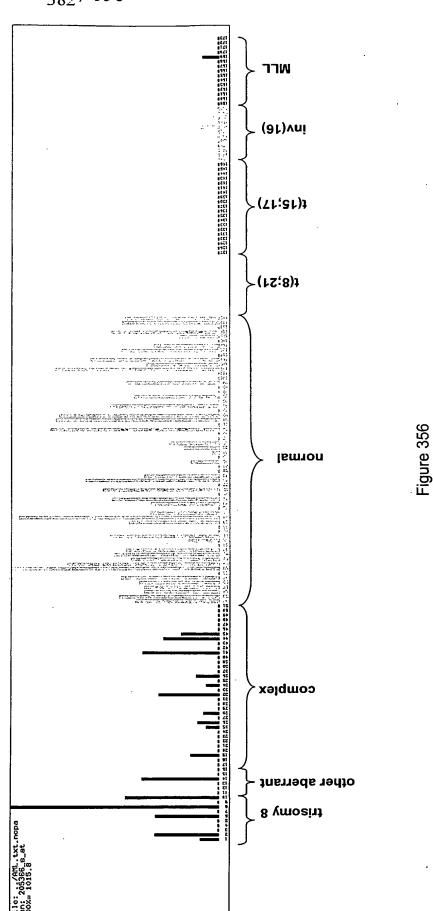
205529\_s\_at, CBFA2T1, AML t(8;21) high

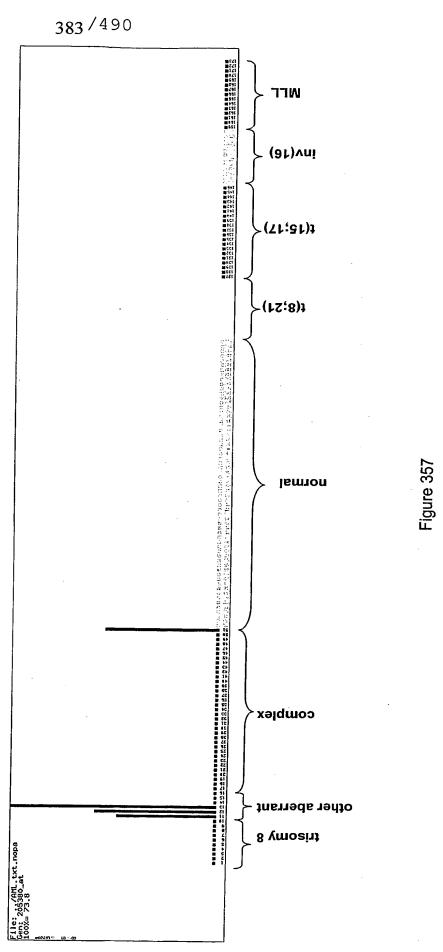


204425\_at, ARHGAP4, AML t(15;17) low



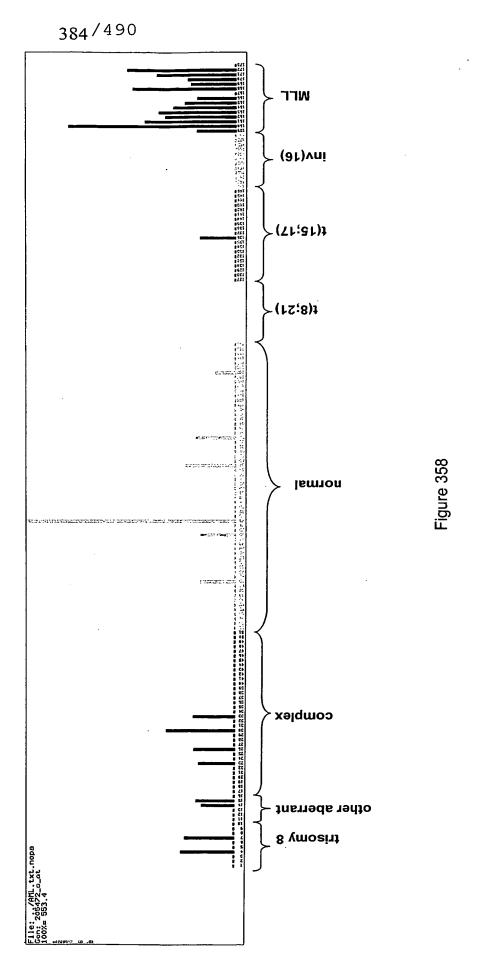
205366\_s\_at, HOXB6, AML t(8;21) low, AML t(15;17) low, AML inv(16) low, AML MLL low

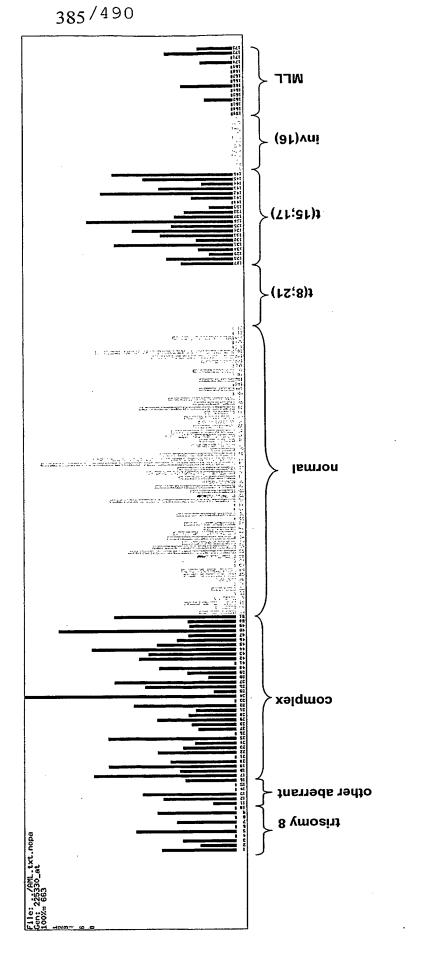




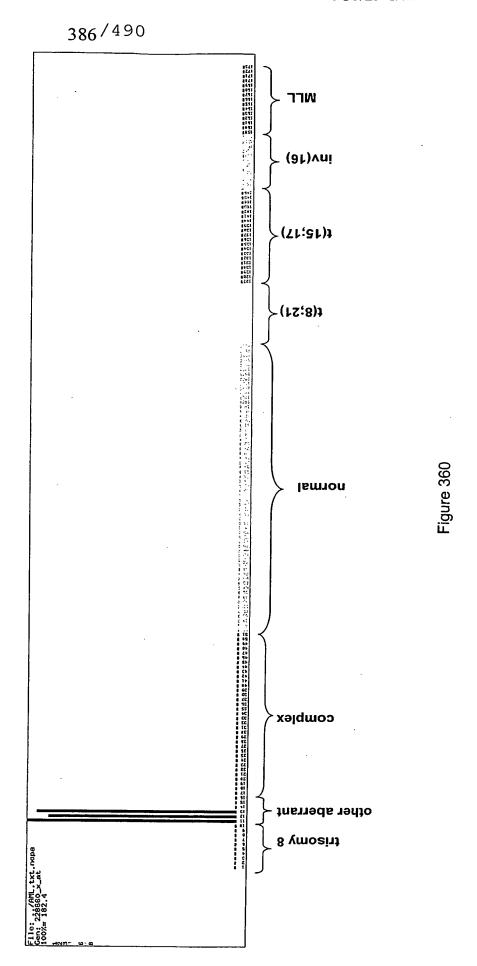
BNSDOCID: <WO\_\_\_\_03039443A2\_I\_>

205472\_s\_at, DACH, AML MLL high





228660\_x\_at, SEMA4F, other high

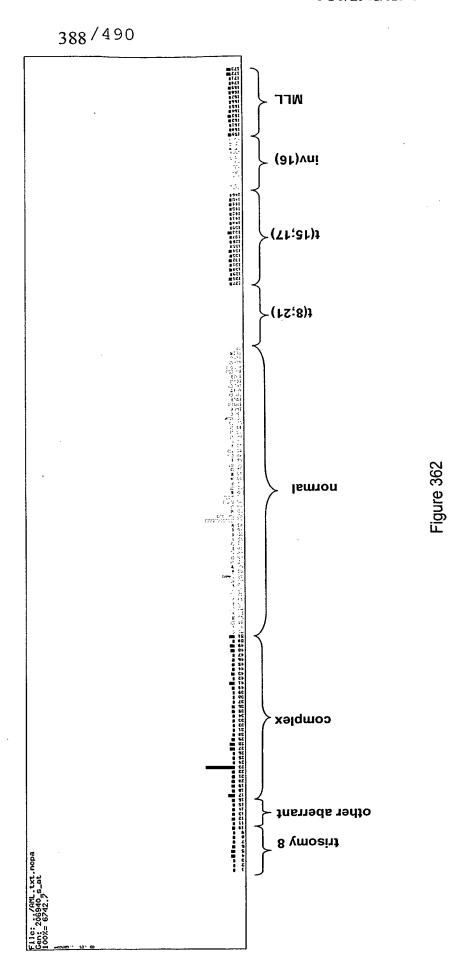


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שרד (8f)vni (42:41) £(8;21) normal complex other aberrant 8 ymosint

206761\_at, TACTILE, AML MLL low

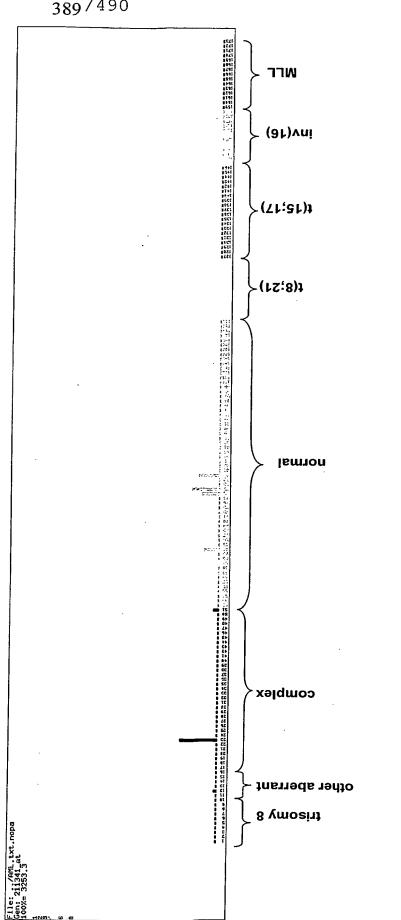
206940\_s\_at, POU4F1, AML t(8;21) high



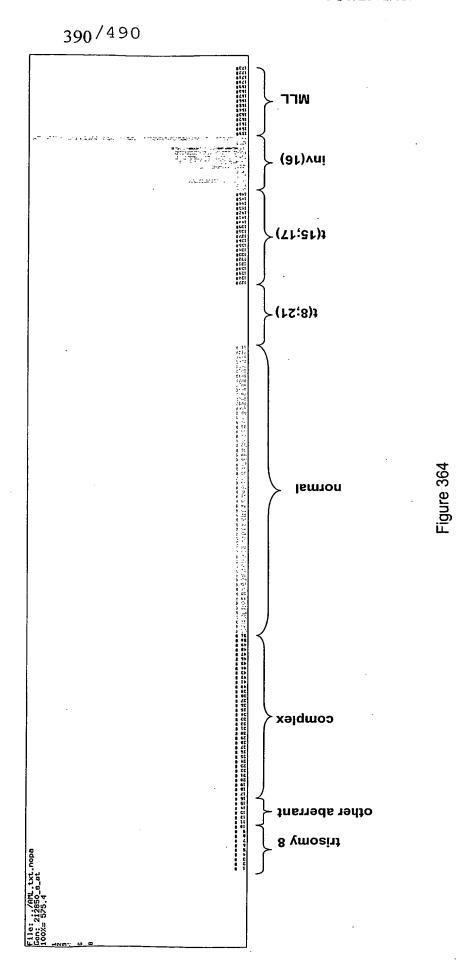
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211341\_at, POU4F1, AML t(8;21) high

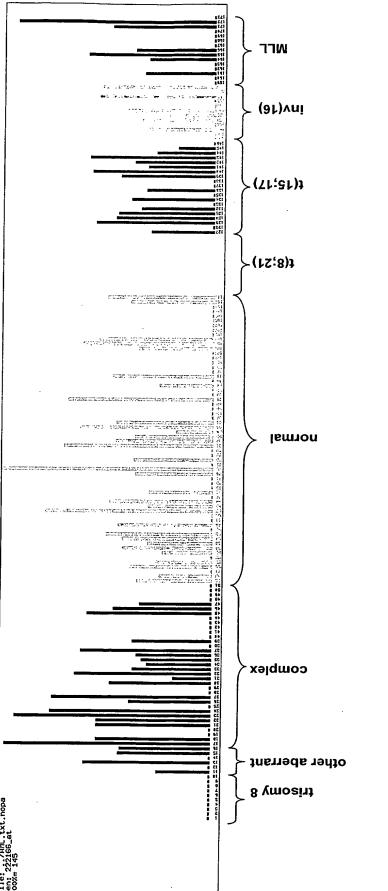
ı



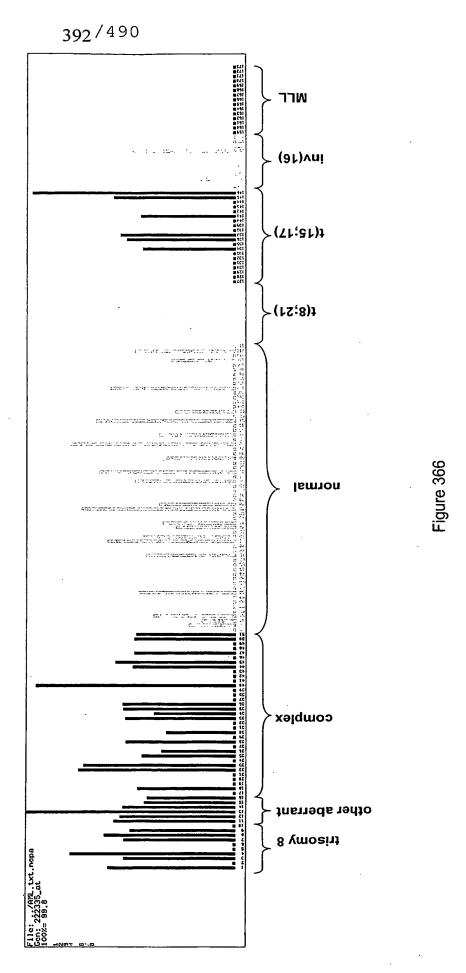
212850\_s\_at, LRP4, AML inv(16) high



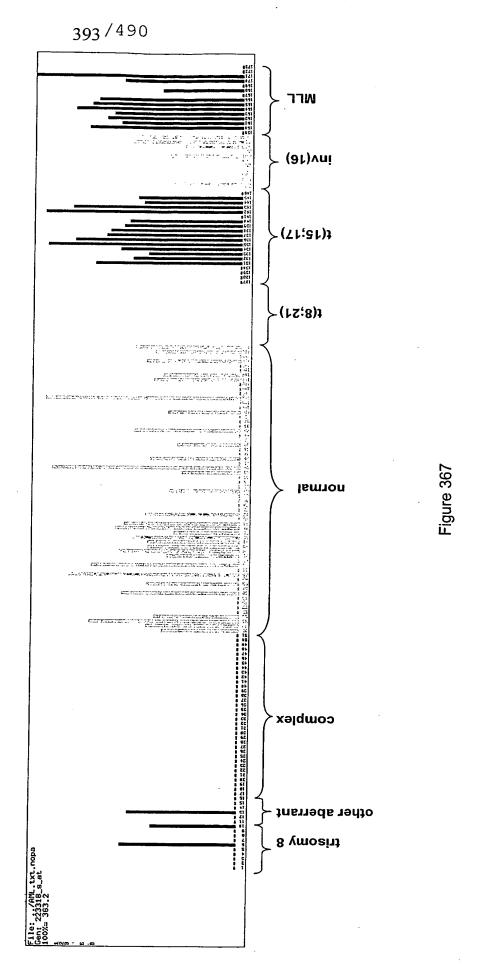
391/490



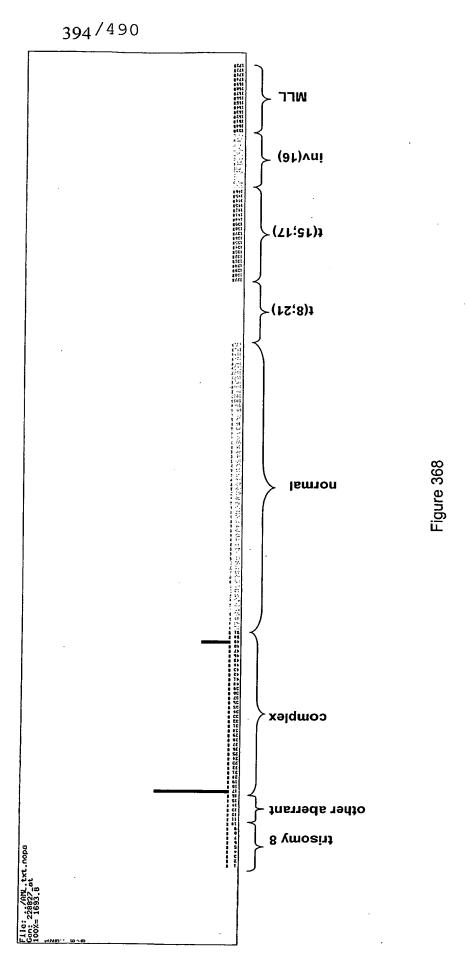
222166\_at, AML +8 low



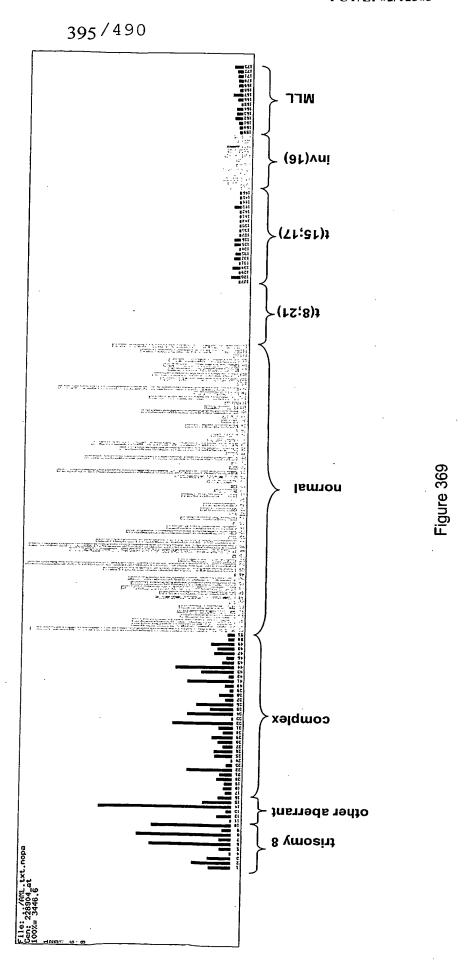
223318\_s\_at, MGC10974, AML complex low



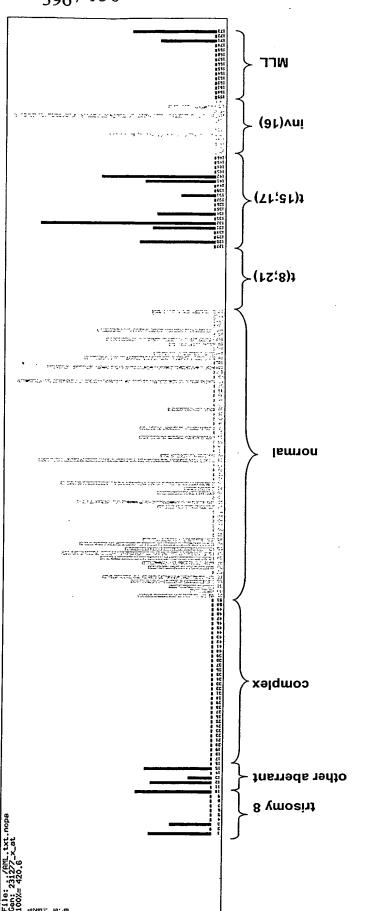
228827\_at, AML t(8;21) high



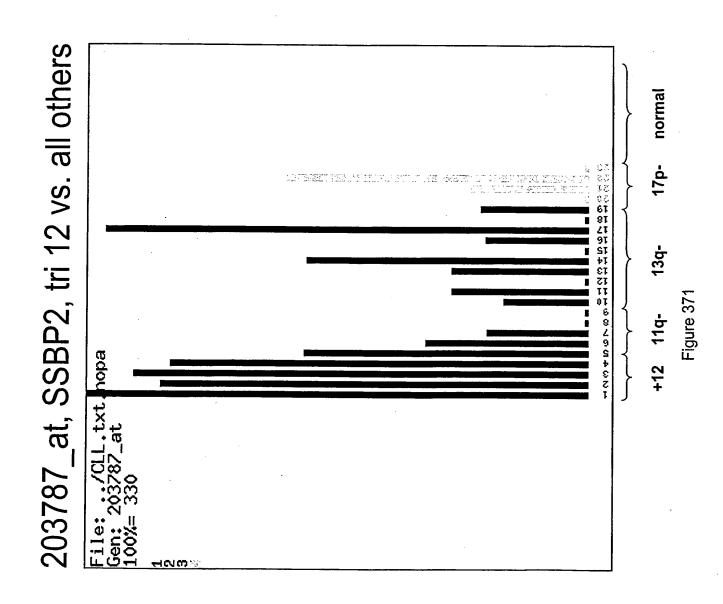
## 228904\_at, AML t(8;21) low, AML t(15;17) low, AML inv(16) low, AML MLL low

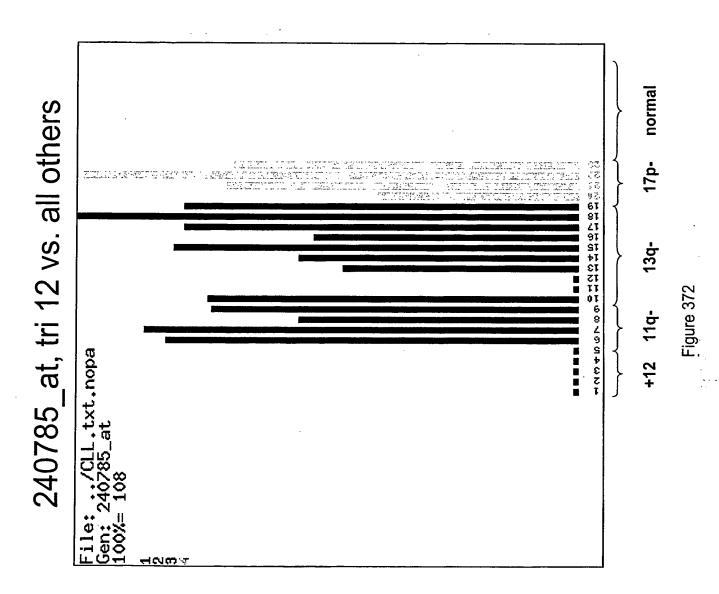


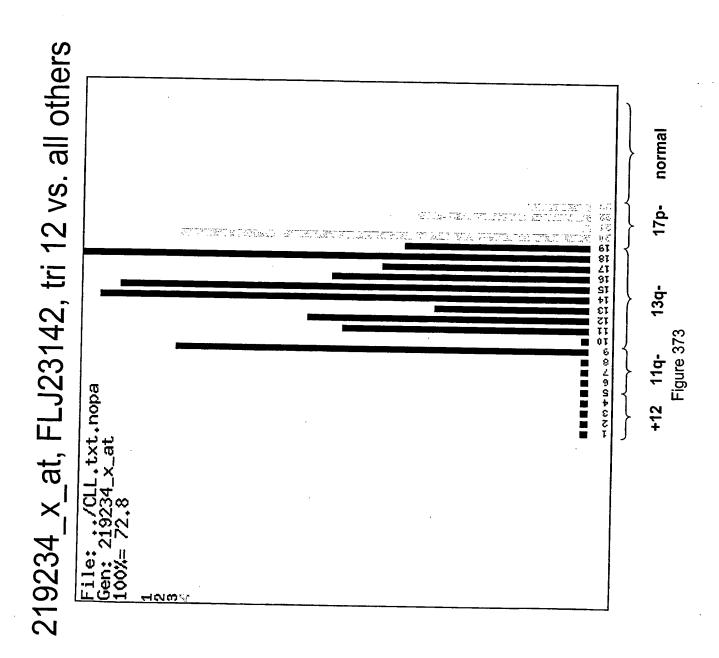
396/490

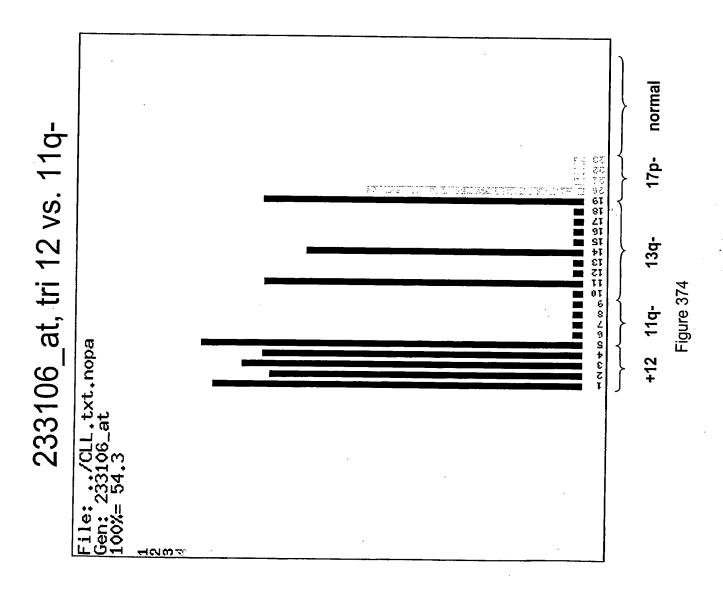


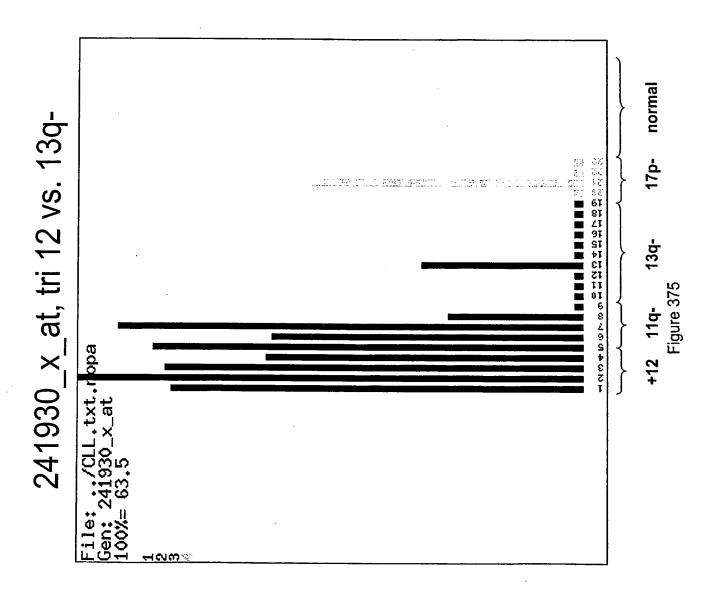
231277\_x\_at, AML complex low

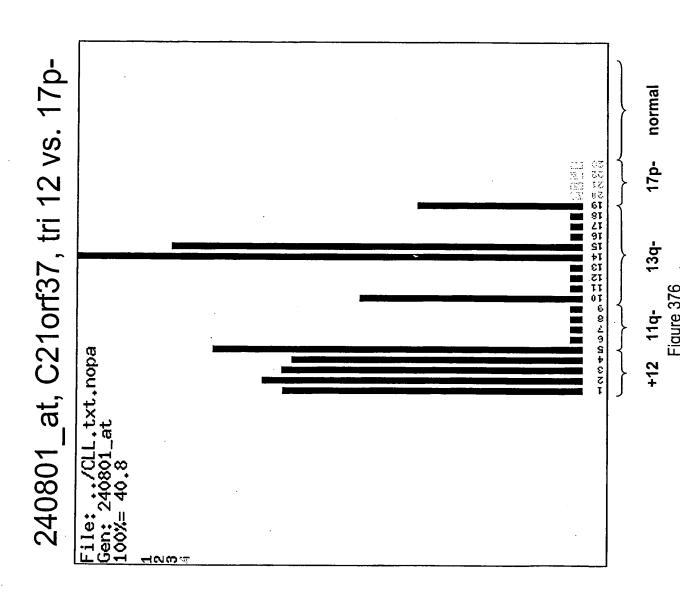


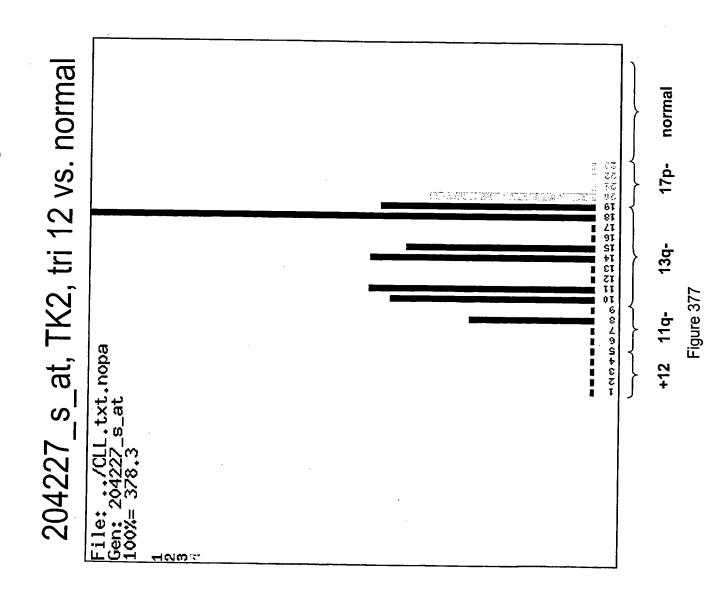


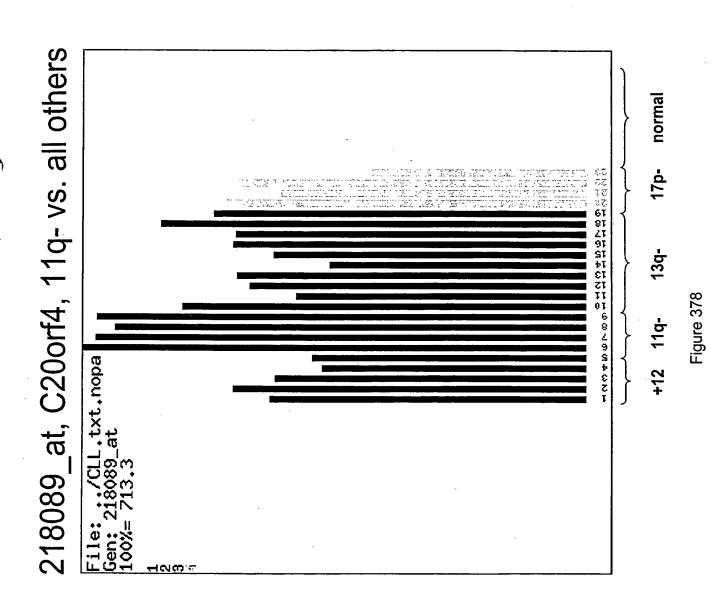




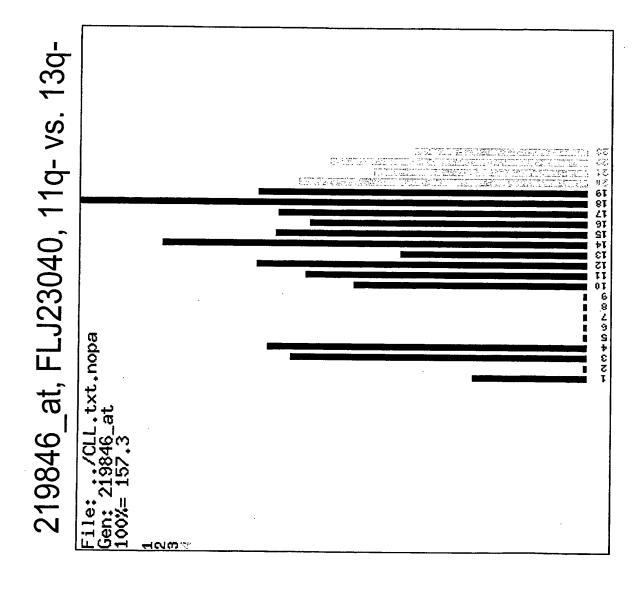


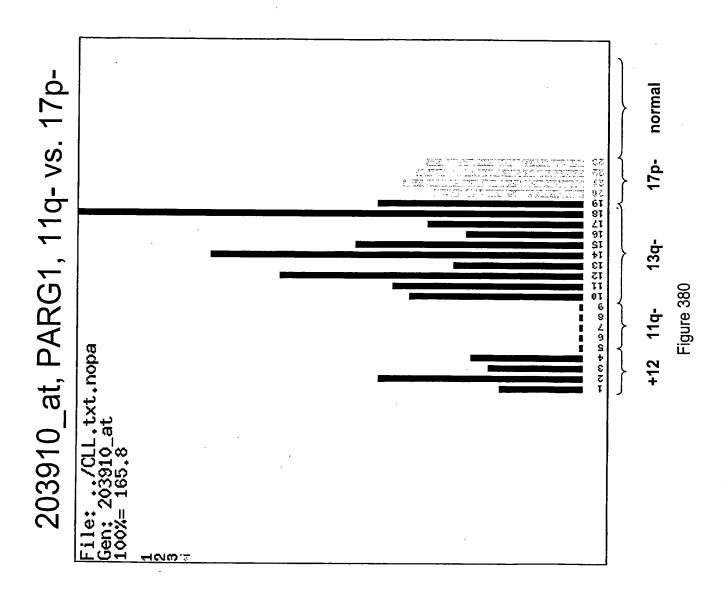


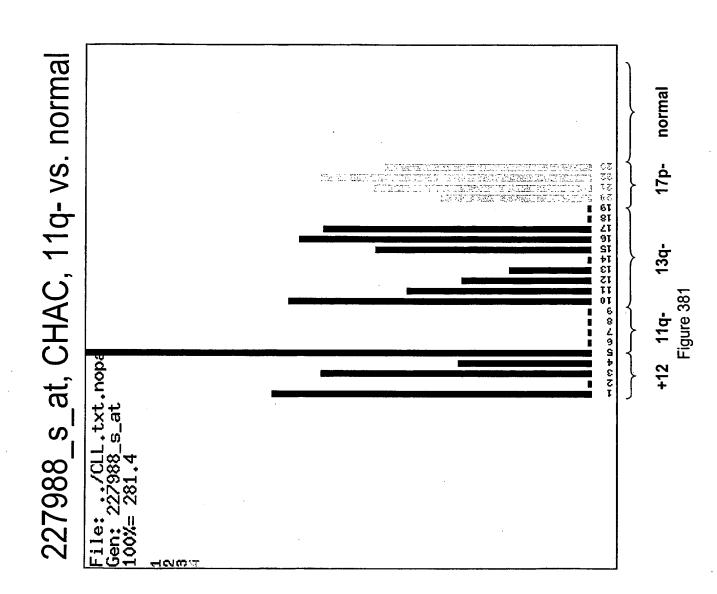


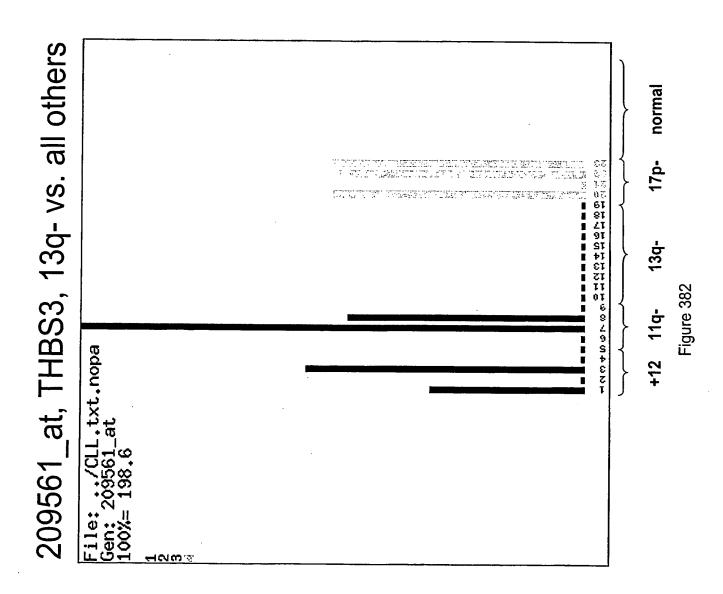


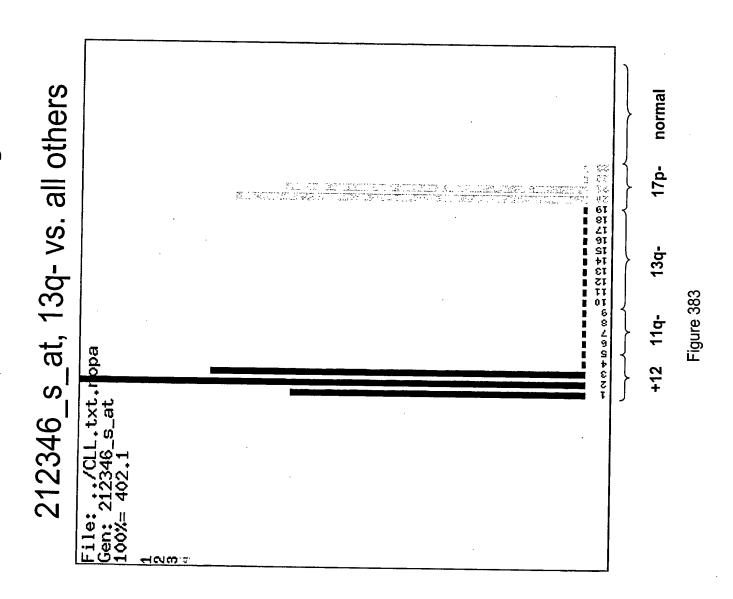


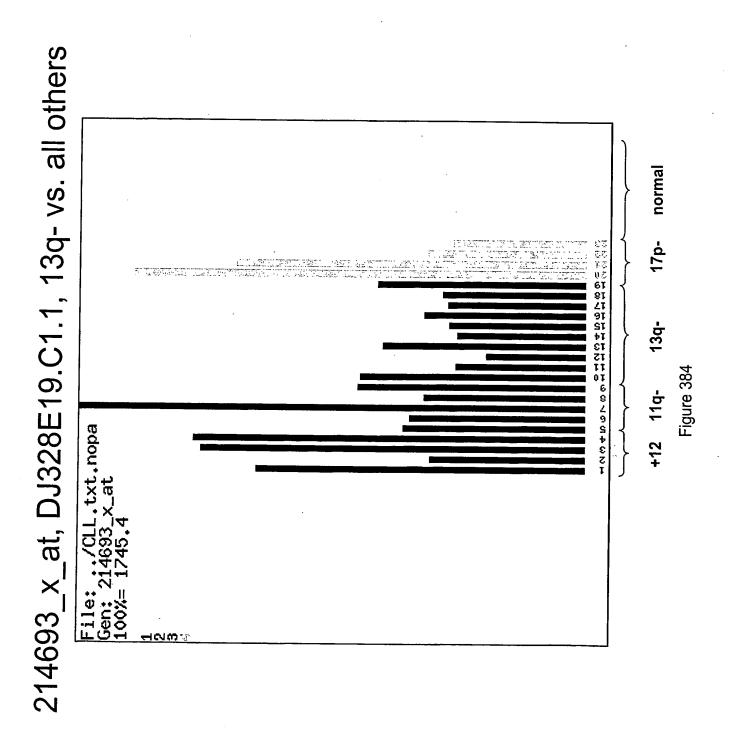


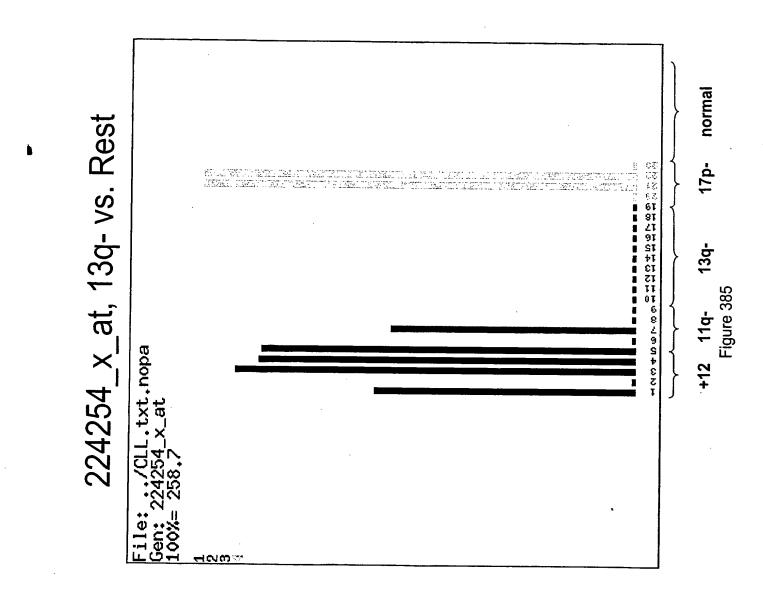


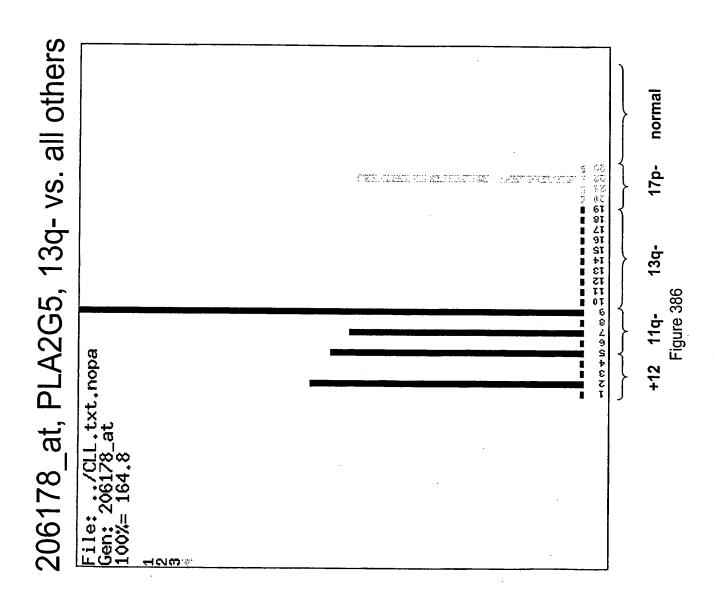


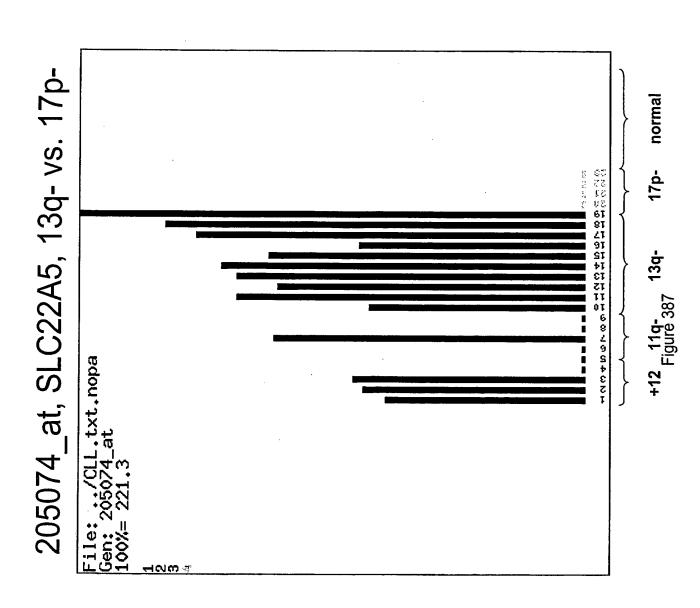


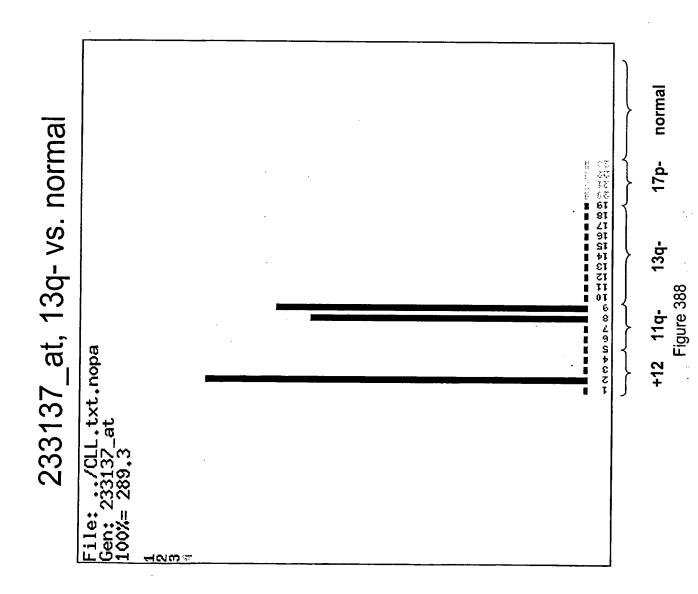


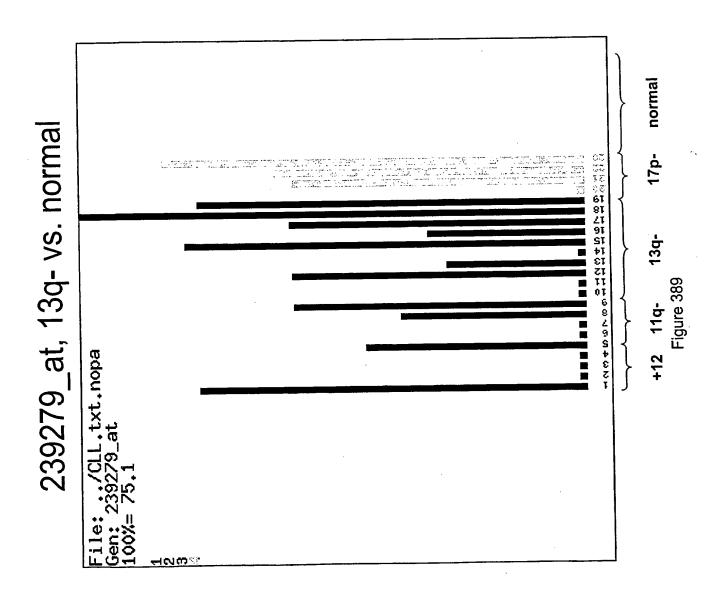


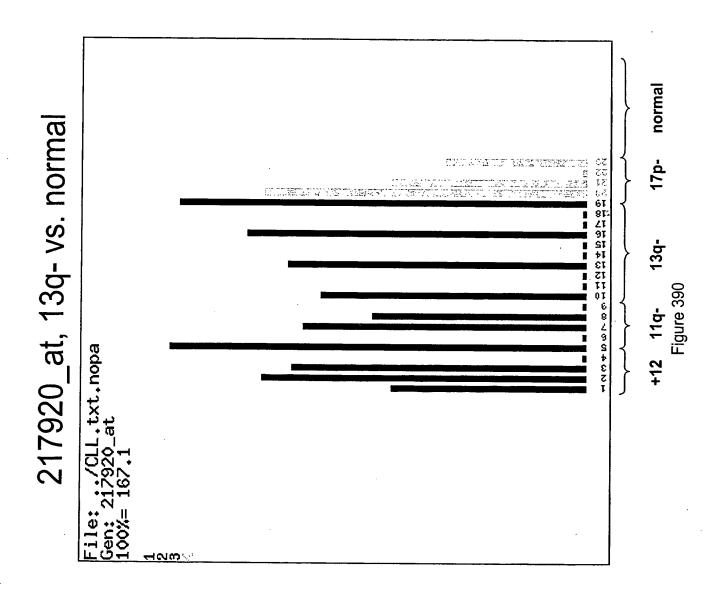


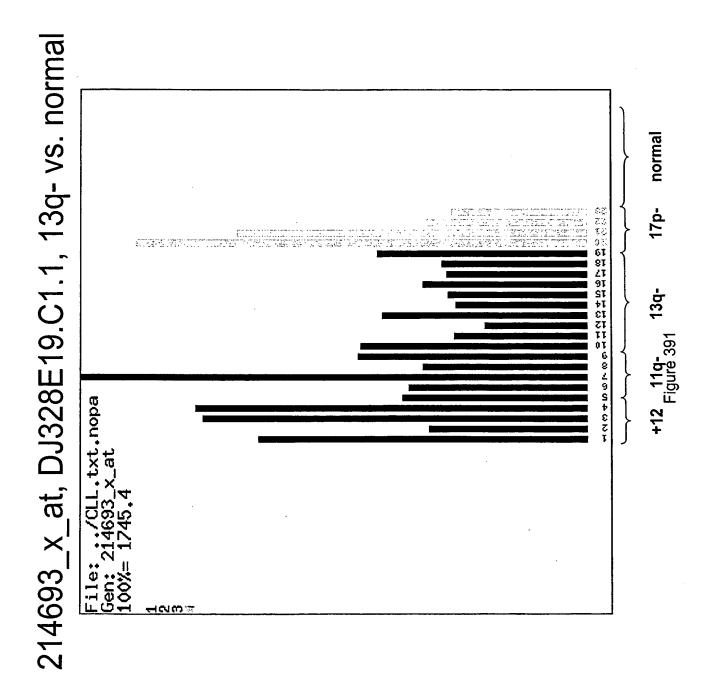


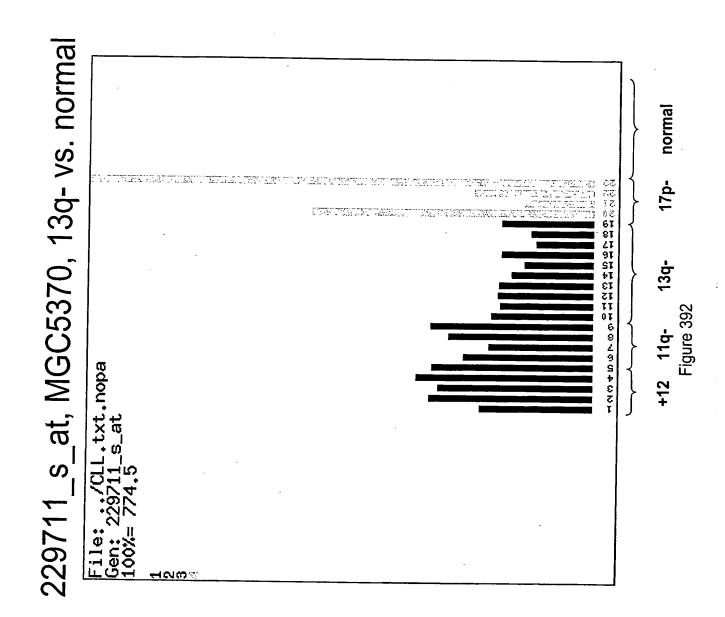


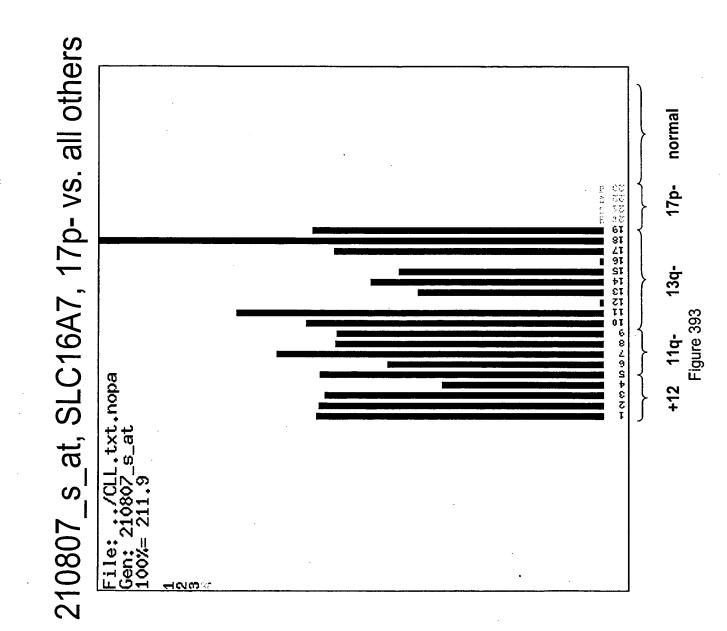


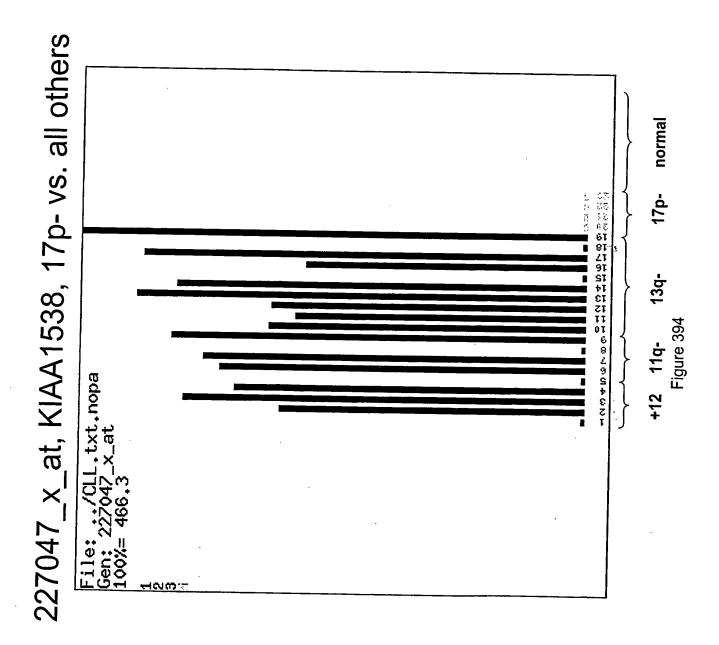


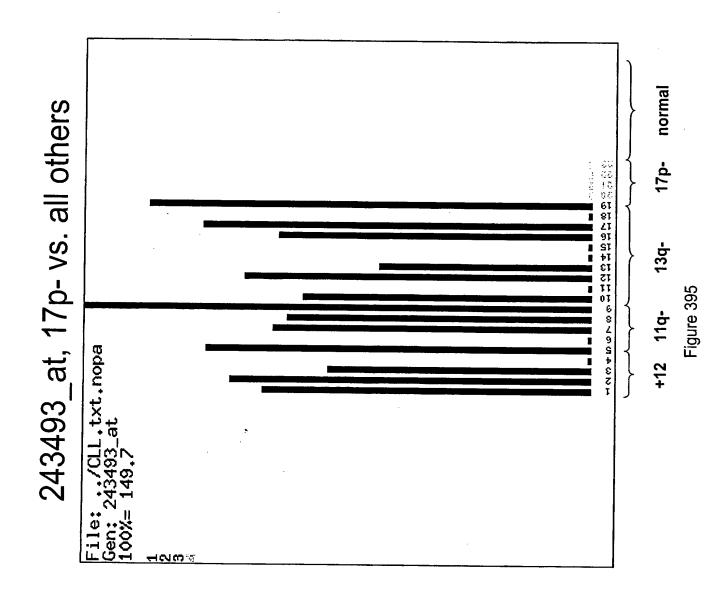


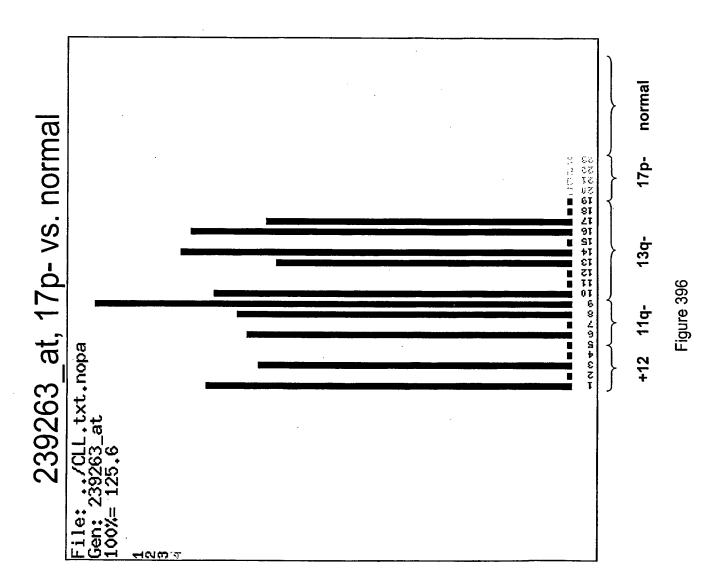


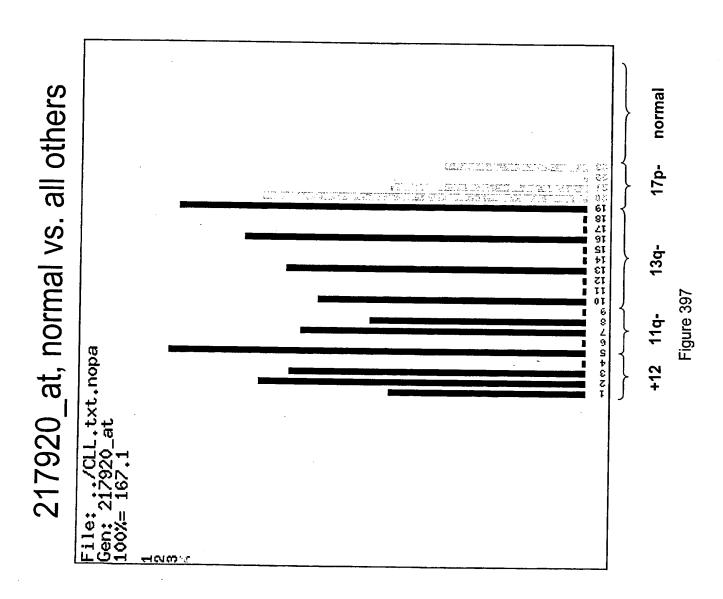


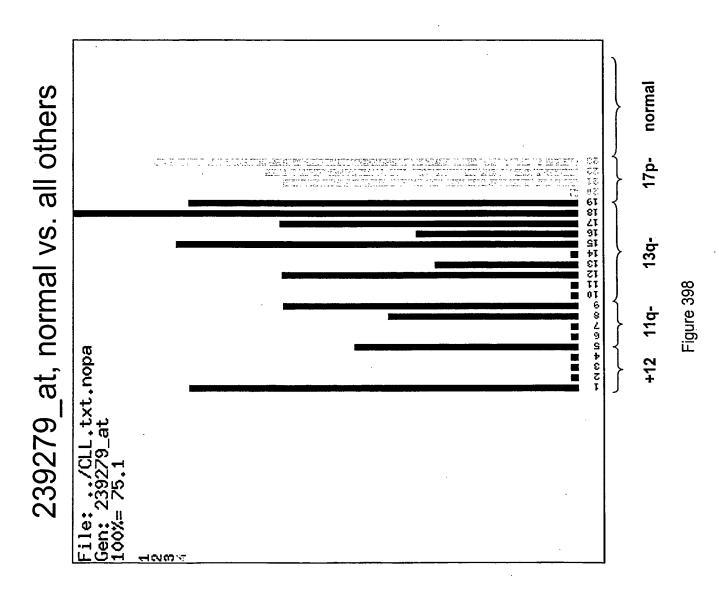


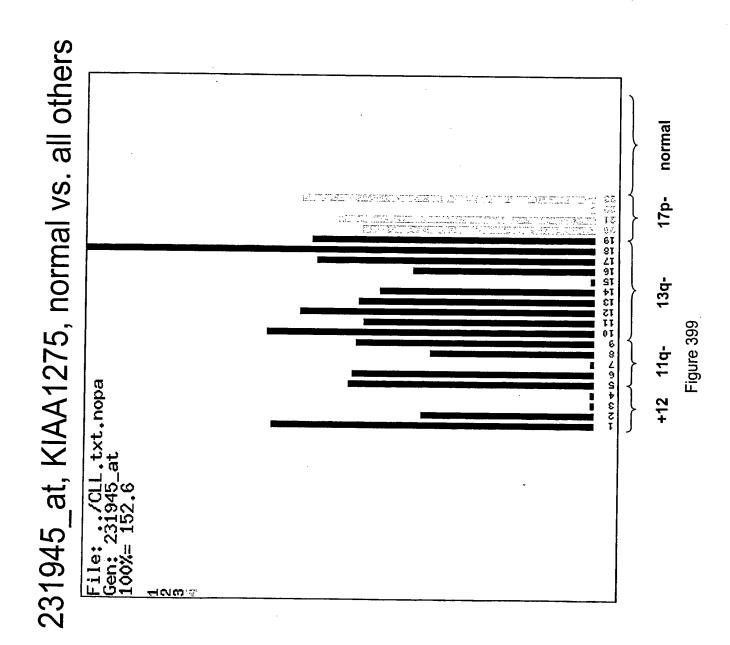


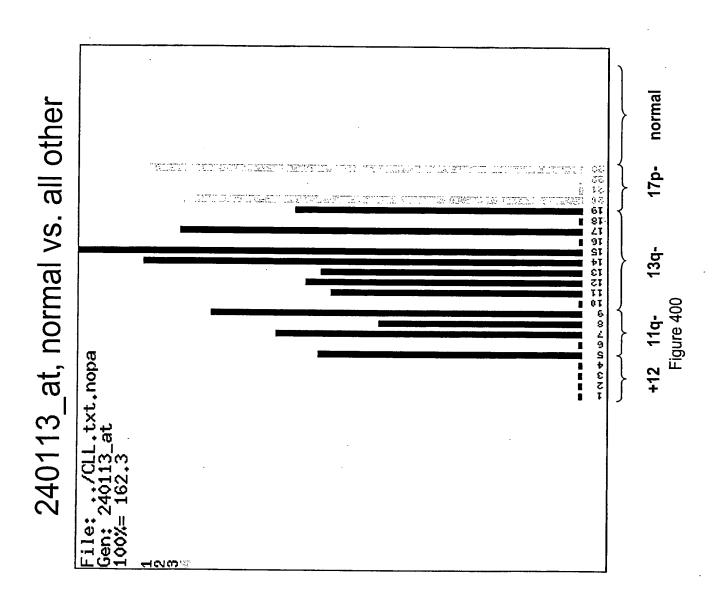


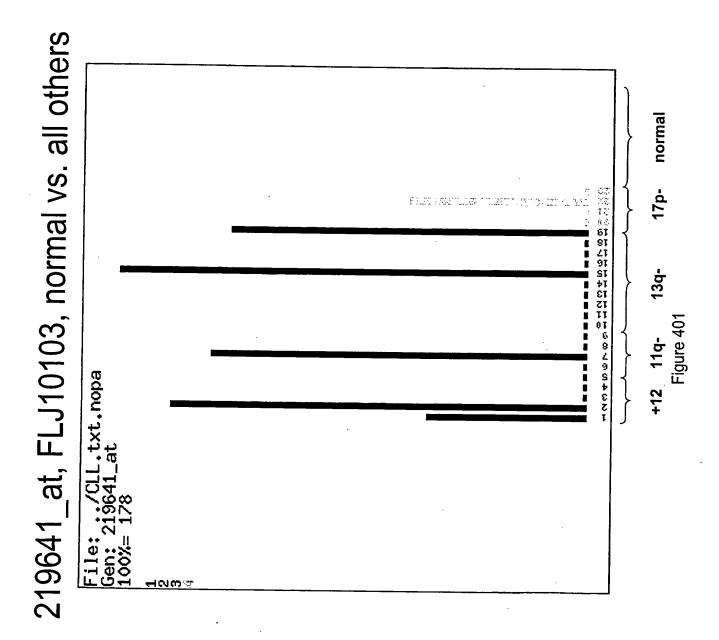


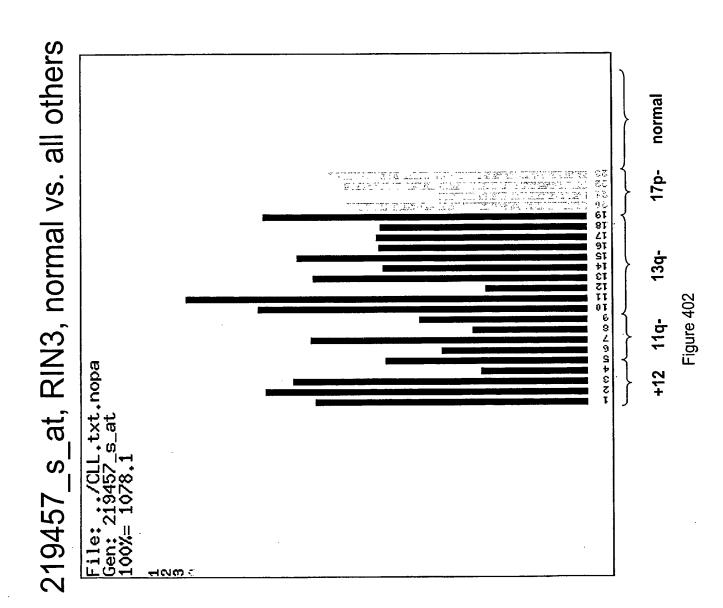


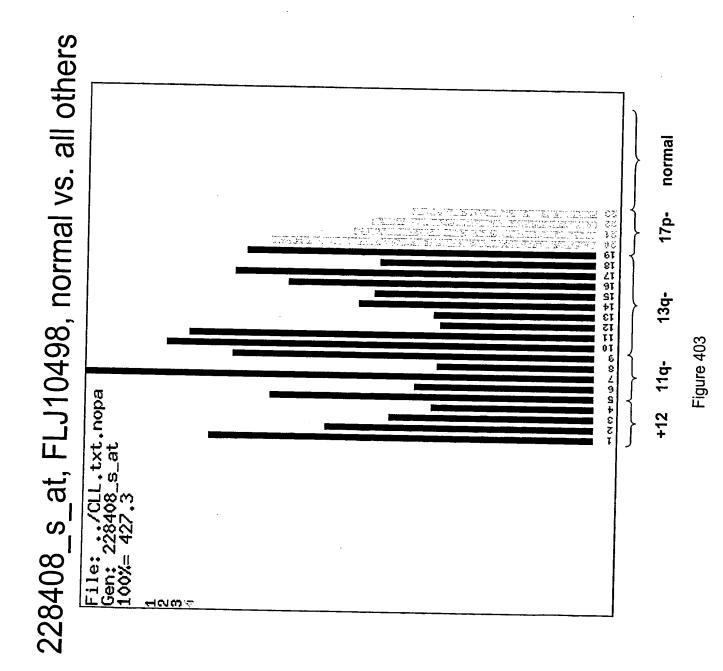


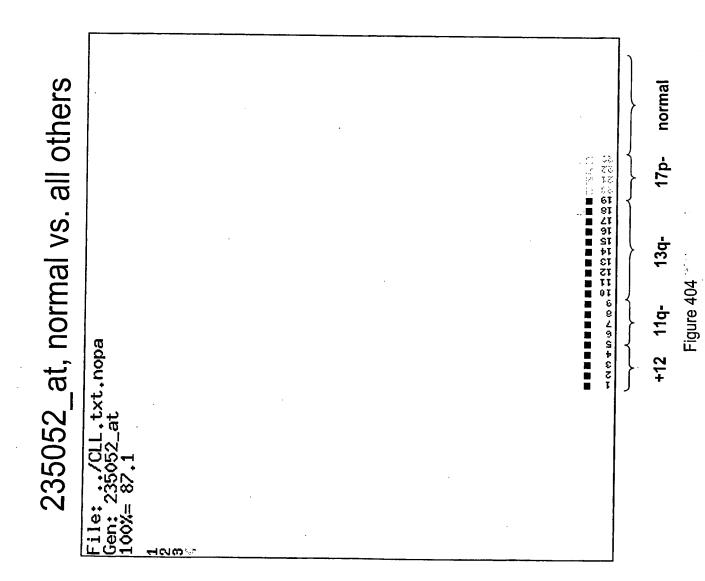






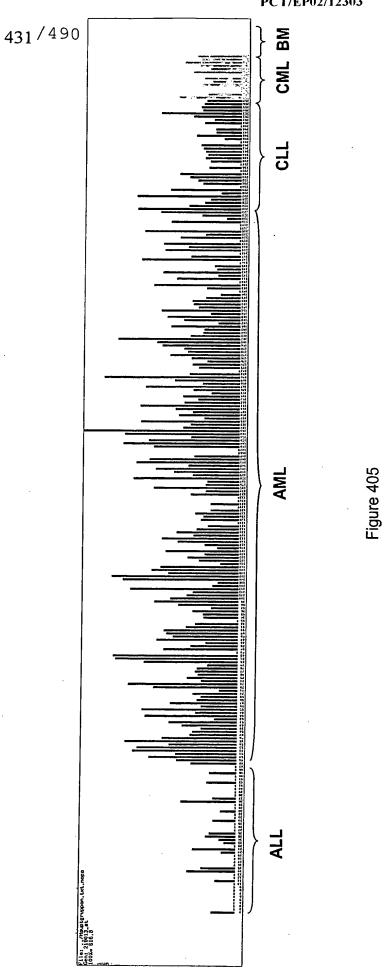






BNSDOCID: <WO\_\_\_\_\_03039443A2\_I\_>

219013\_at, FLJ21634, ALL vs. all others



243362\_s\_at, LEF1, ALL vs. all others

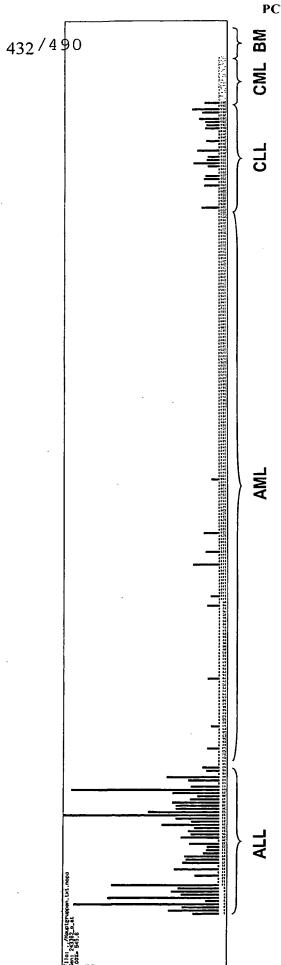
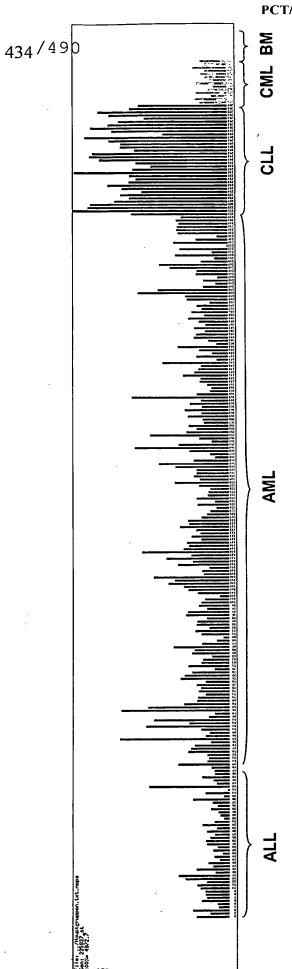


Figure 4

204215\_at, MGC4175, ALL vs. AML

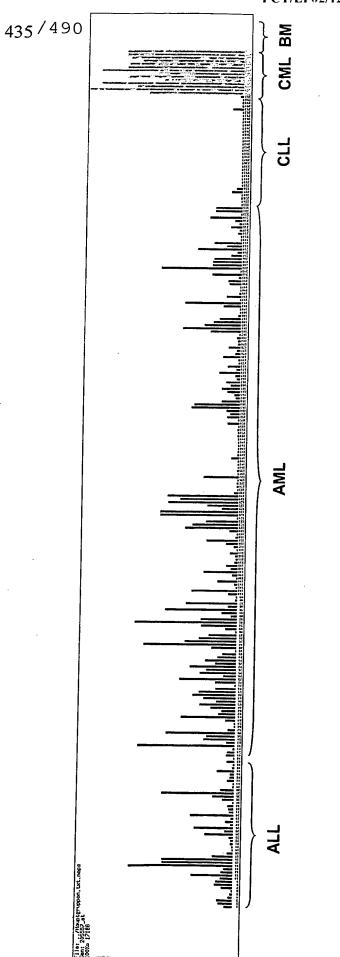


225927\_at, MAP3K1, ALL vs. CLL



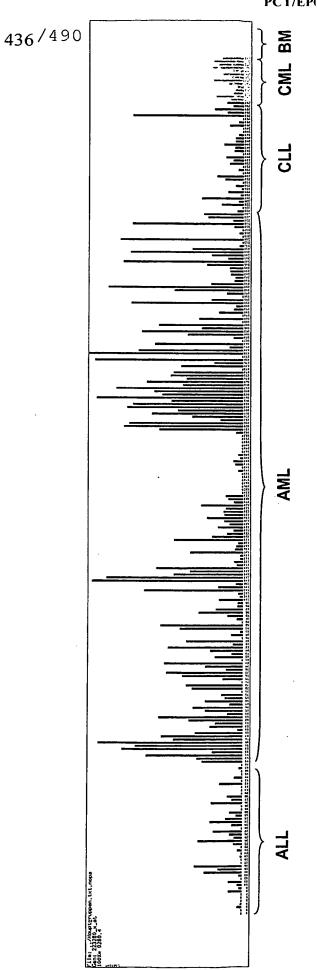
BNSDOCID: <WO\_\_\_\_\_03039443A2\_I\_>

205557\_at, BPI, ALL vs. CML



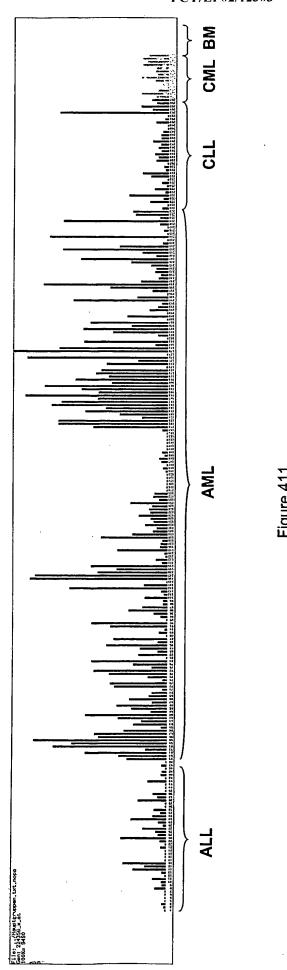
Figure

223280\_x\_at, MS4A6A, ALL vs. normal BM



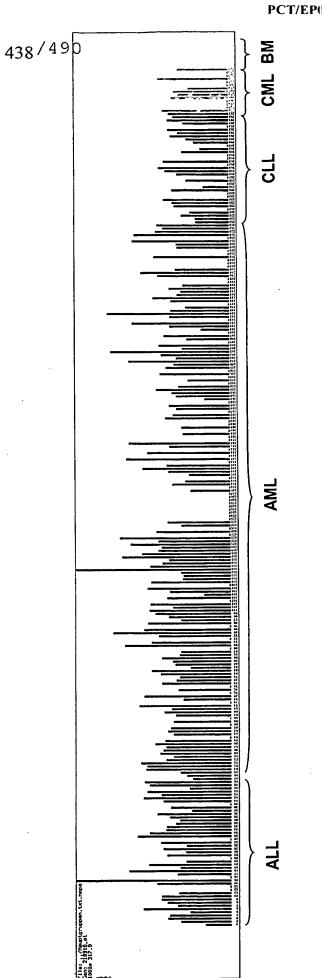
BNSDOCID: <WO\_\_\_\_03039443A2\_I\_>

224356\_x\_at, MS4A6A, ALL vs. normal BM



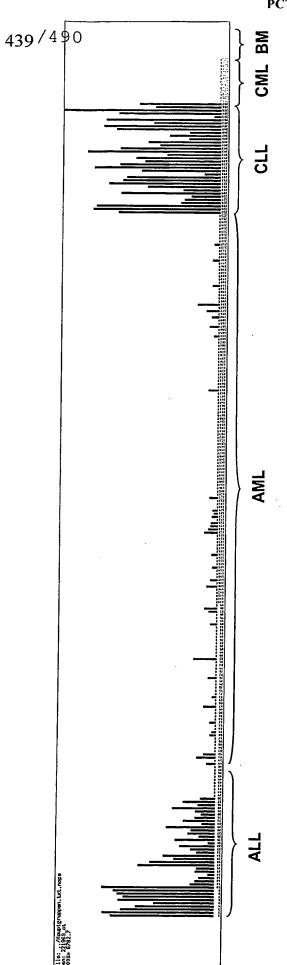
BNSDOCID: <WO 03039443A2 L >

218916\_at, FLJ23436, ALL vs. normal BM



BNSDOCID: <WO\_\_\_\_03039443A2\_I\_>

221969\_at, PAX5, AML vs. all others



206398\_s\_at, CD19, AML vs. Rest

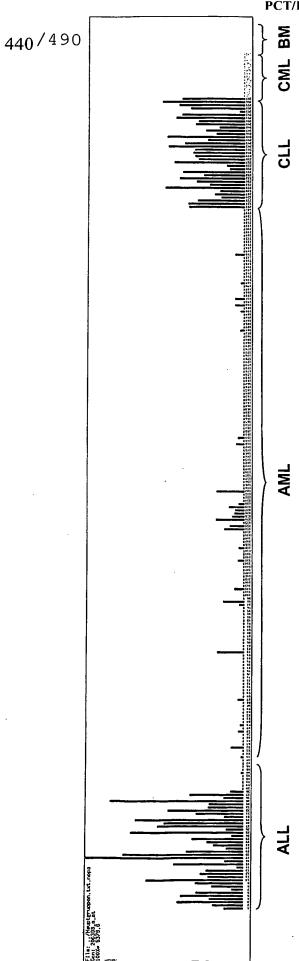
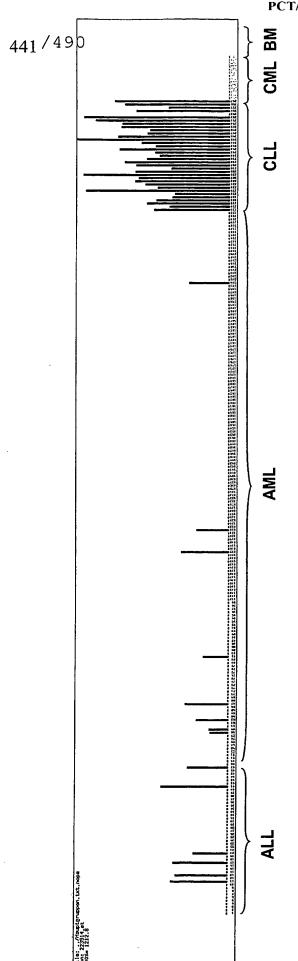


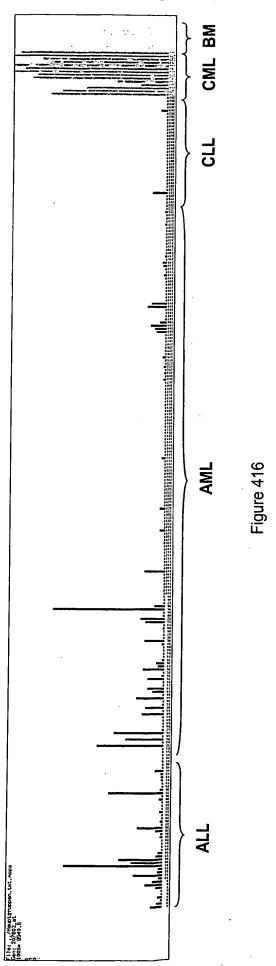
Figure 414

223514\_at, CARD11, AML vs. CLL

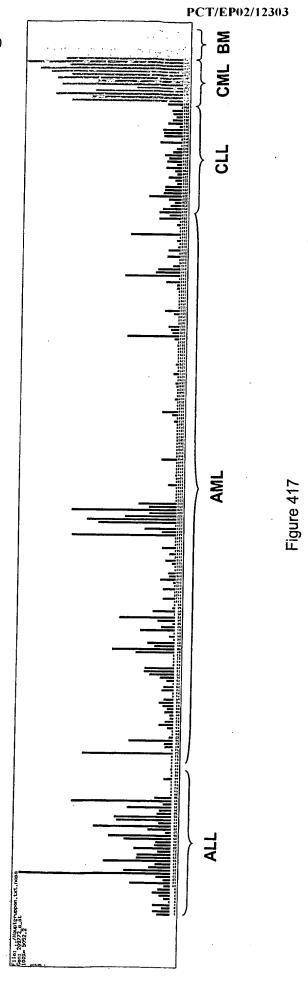


BNSDOCID: <WO\_\_\_\_03039443A2\_I\_>

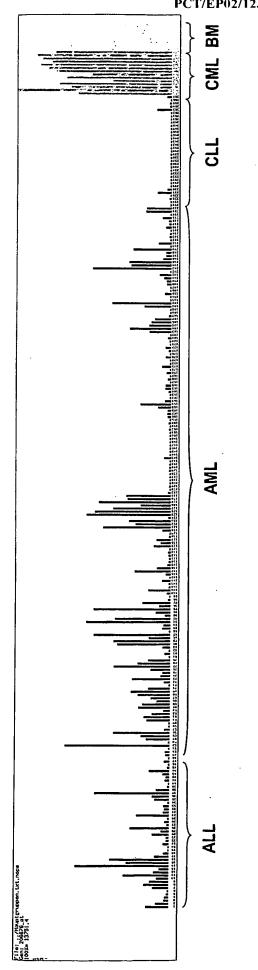
207802\_at, SGP28, AML vs. CML



209772\_s\_at, CD24, AML vs. CML



206676\_at, CEACAM8, AML vs. CML



203936\_s\_at, MMP9, AML vs. CML

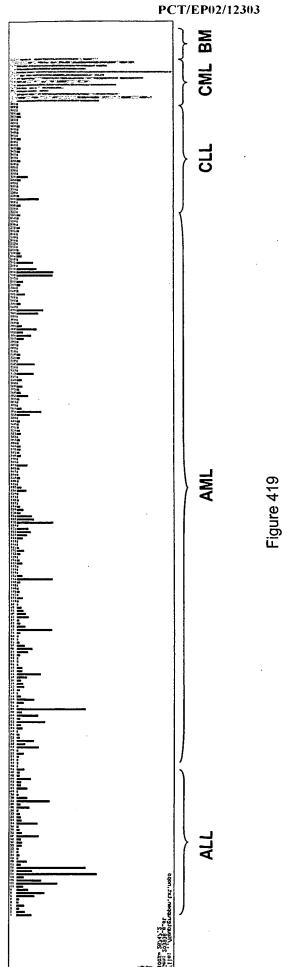
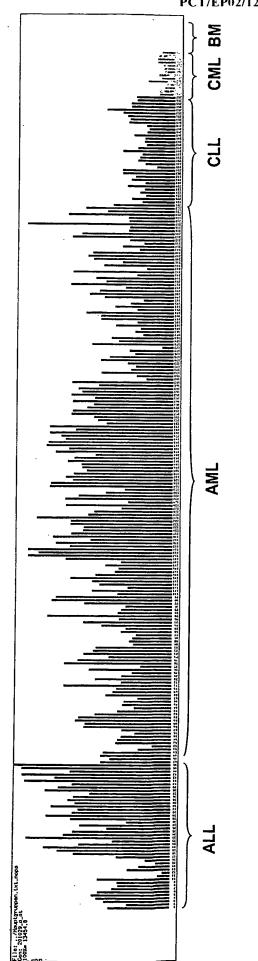


Figure 420

201029\_s\_at, MIC2, AML vs. CML





BM CML CLL AML

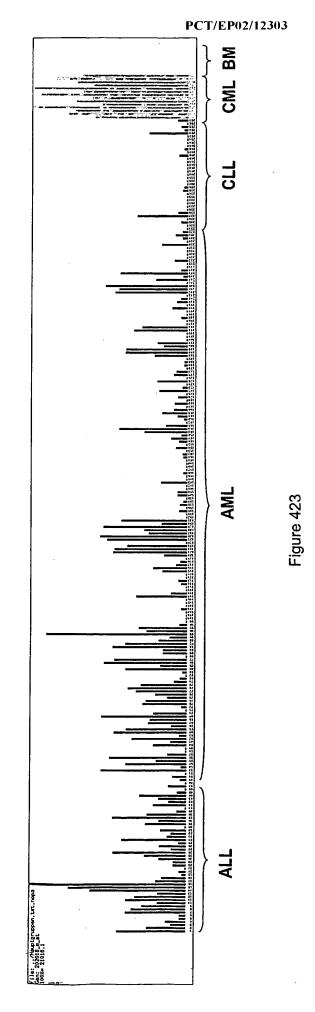
223894\_s\_at, FTS, AML vs. CML



CML BM

207269\_at, DEFA4, AML vs. CMI

202018\_s\_at, LTF, AML vs. normal BM



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CLL

**AML** 

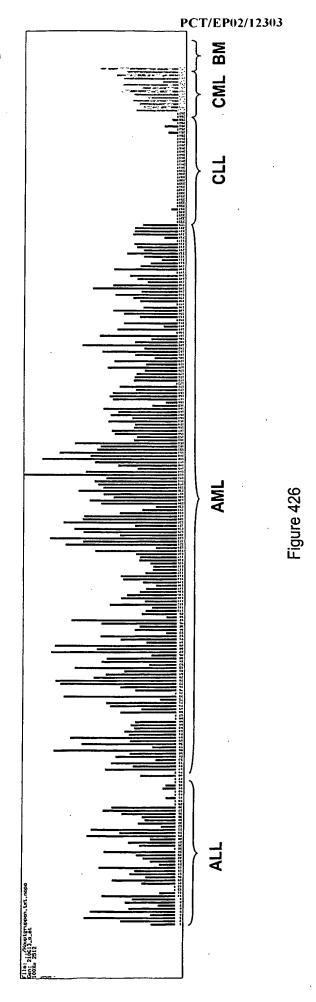
ALL



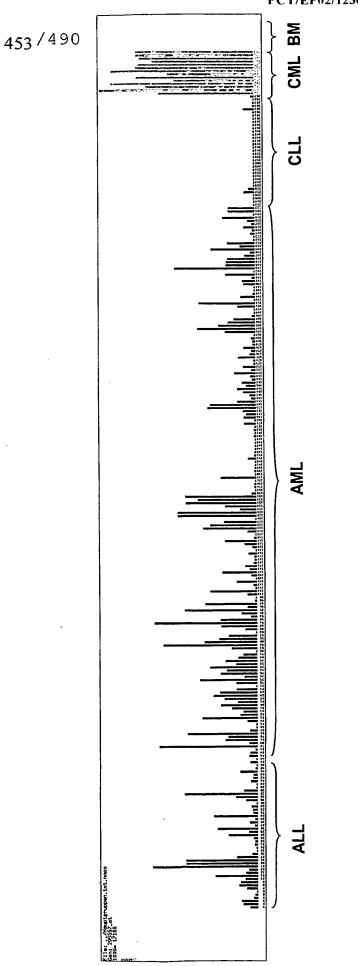
CML BM

210254\_at, CLL vs. CML

210613\_s\_at, SYNGR1, CLL vs. normal BM



205557\_at, BPI, CML vs. all others

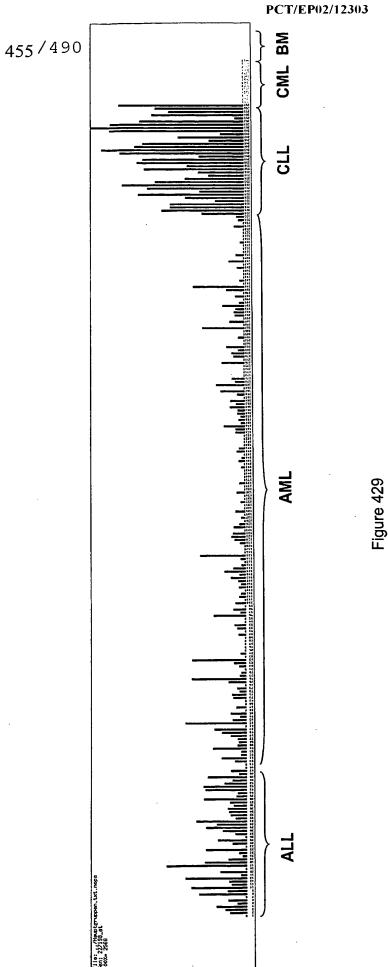


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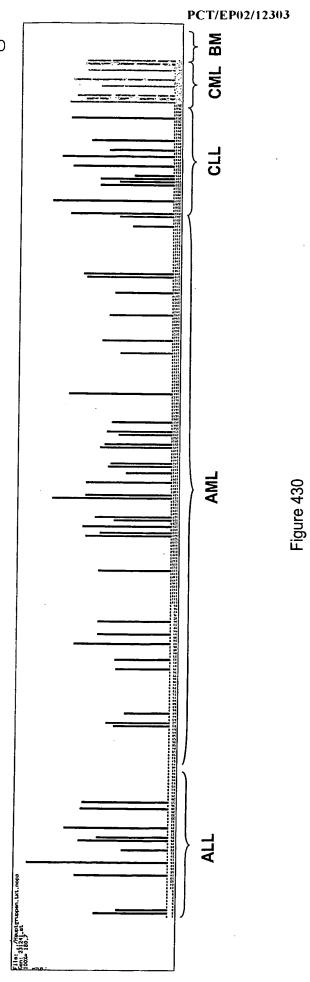
CML BM CLL AML Figure 428

209772\_s\_at, CD24, CML vs. all others

227198\_at, CML vs. normal BM



231241\_at, normal BM vs. all others



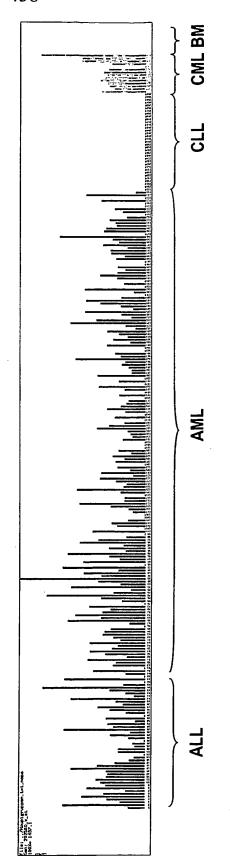


CML BM

227497\_at, normal BM vs. all others

202580\_x\_at, FOXM1, CLL

Figure 432



202709\_at, FMOD, CLL

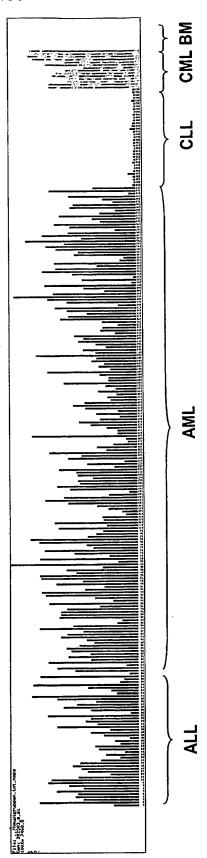
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CML BM CLL AML ALL

Journe 433

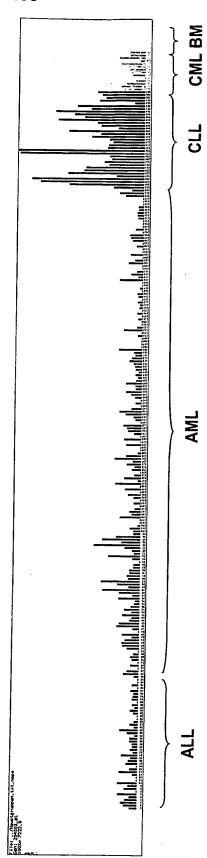
202503\_s\_at, KIAA0101, CLL

Figure 434



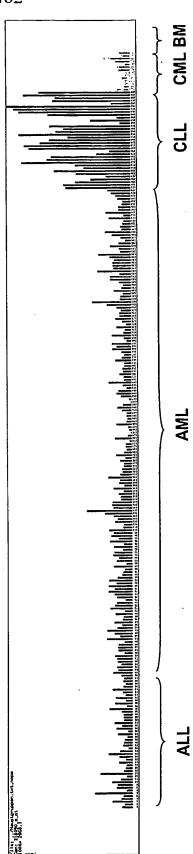
BNSDOCID: <WO\_\_\_\_03039443A2\_I\_>

204882\_at, KIAA0053, CLL



-igure 435

Figure 436



211352\_s\_at, NCOA3, CLL

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CLL AML ALL

Figure 437

217950\_at, NOSIP, CLL

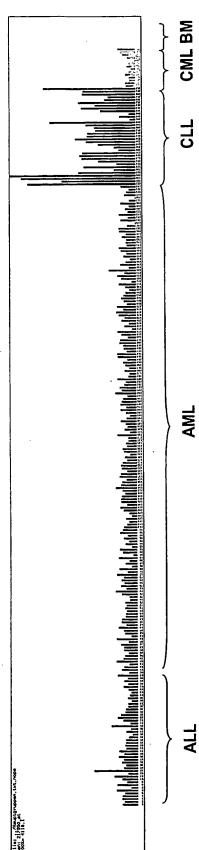
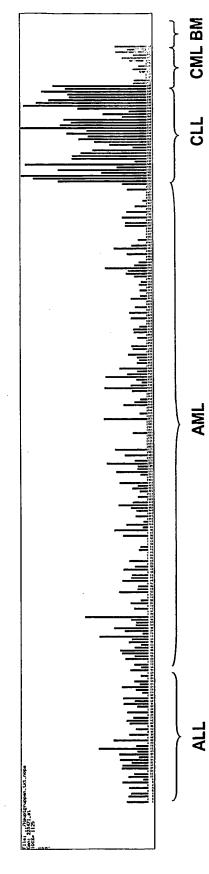


Figure 438



228471\_at, CLI

226147\_s\_at, CLL

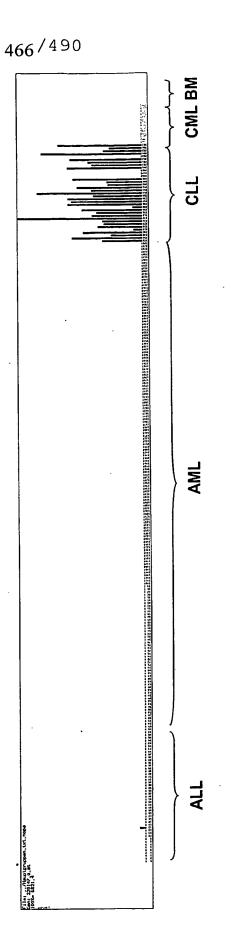


Figure 440

239287\_at, CLI

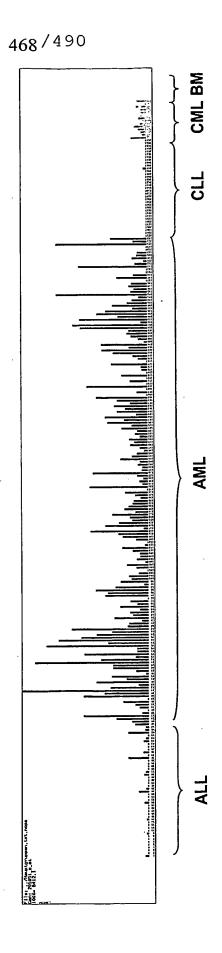
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CML BM CLL **AML** 

Figure 44'

Figure 442

205051\_s\_at, KIT, AML



214761\_at, OAZ, ALL

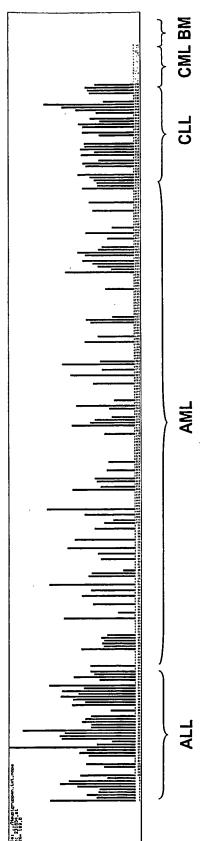
469/490

CML BM CL AML

Figure 44

231854\_at, CML

Figure 444



BNSDOCID: <WO\_\_\_\_\_03039443A2\_1\_>

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211404\_s\_at, APLP2, AML

CML BM CLL AML ALL

Figure 445

205382\_s\_at, DF, AML high

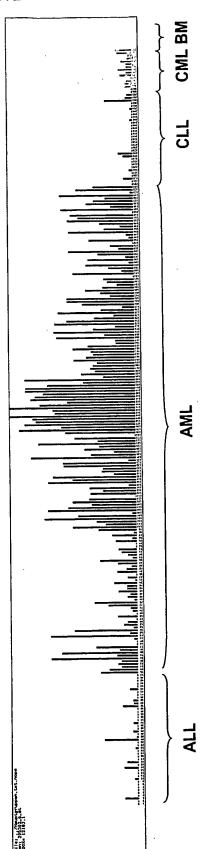


Figure 446

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205599\_at, TRAF1, CML absent, CLL high

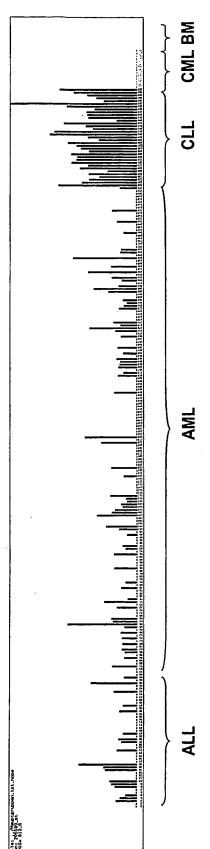


Figure 447

Figure 448



CML BM CLL AML ALL

210948\_s\_at, LEF1, lymphatic high

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206398\_s\_at, CD19, lymphatic high

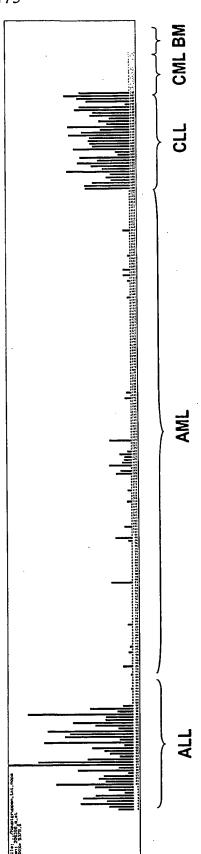


Figure 440

229487\_at, ALL high

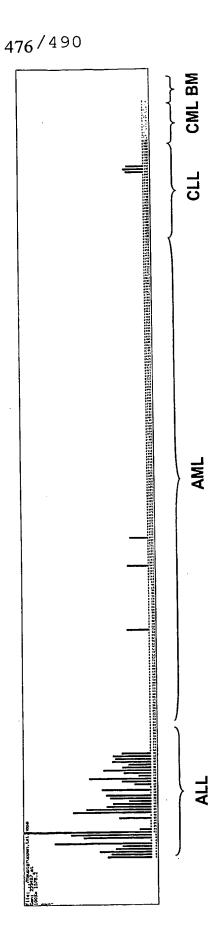
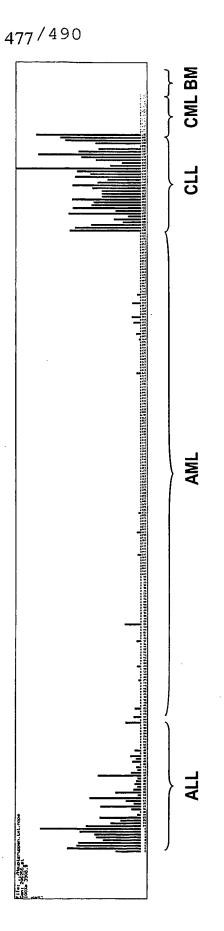


Figure 450

206255\_at, BLK, lymphatic high



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243362\_s\_at, LEF1, ALL high

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CML BM CLL AML ALL

Figure 45

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205049\_s\_at, CD79A, lymphatic high

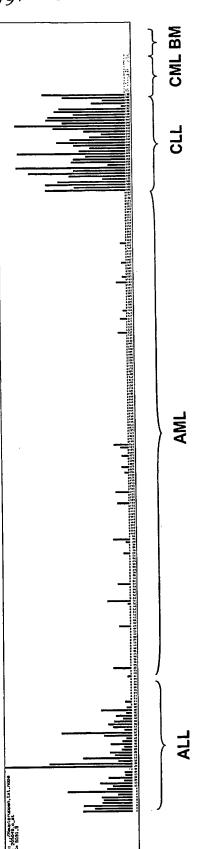
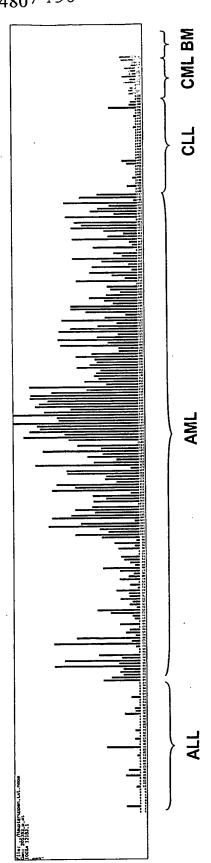


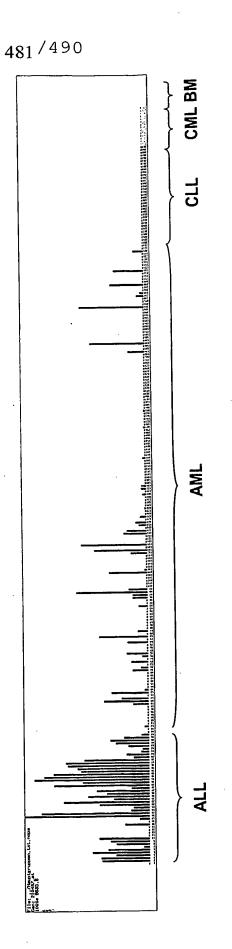
Figure 453

205382\_s\_at, DF, AML high

Figure 454



210487\_at, DNTT, ALL high



Eighre 450

218516\_s\_at, FLJ20421, normal BM absent

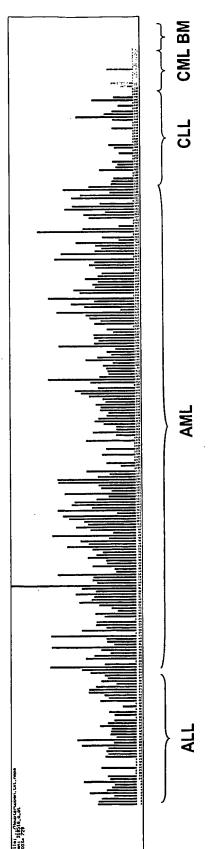


Figure 456

218916\_at, FLJ23436, normal BM absent

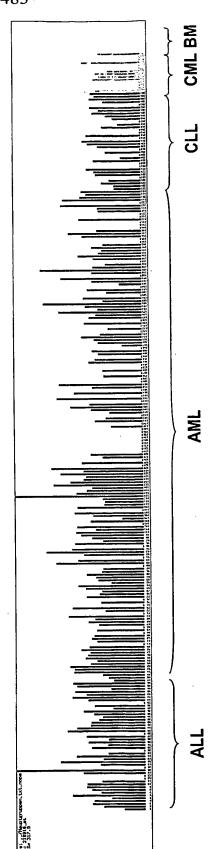


Figure 457

219753\_at, STAG3, ALL high

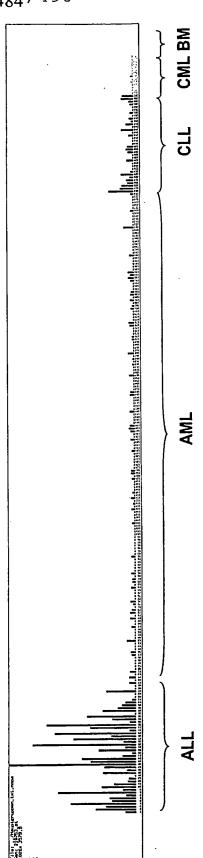


Figure 458

221969\_at, PAX5, lymphatic high

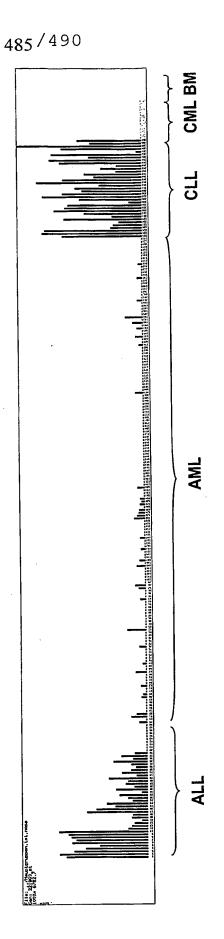


Figure 459

223703\_at, CDA017, myeloid and BM high

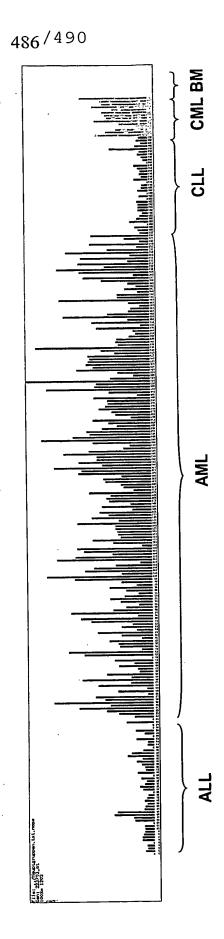


Figure 460

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243363\_at, LEF1, lymphatic high

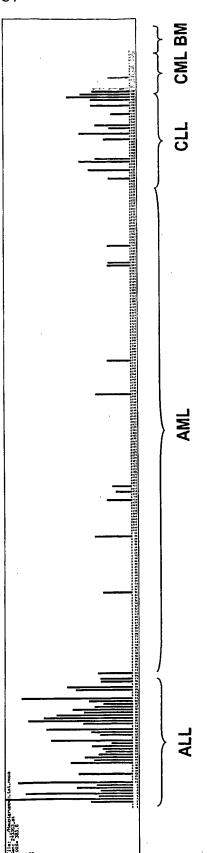


Figure 461

41577\_at, PPP1R16B, CML low

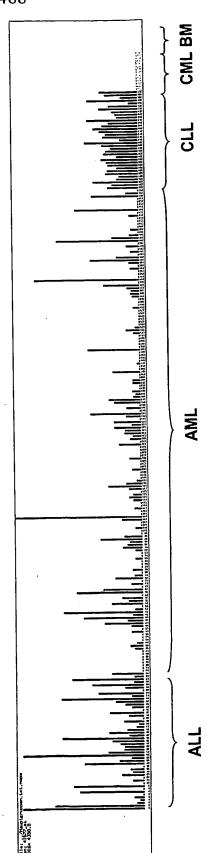


Figure 462

229790\_at, TERF2, CML, BM low

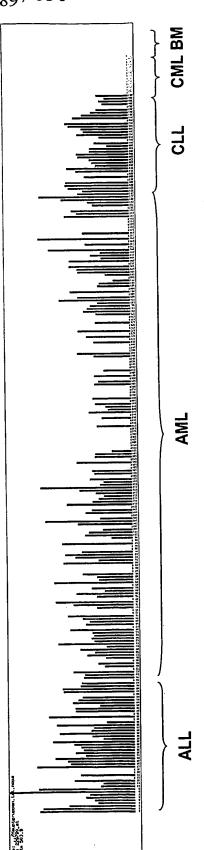


Figure 463

231736\_x\_at, MGST1, myeloid and BM high

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CL AML

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